

OM protein - protein search, using sw model

Run on: August 23, 2004, 16:47:23 ; Search time 127 Seconds
 (without alignments)
 705.256 Million cell updates/sec

Title: US-09-891-138A-2
 Perfect score: 1650
 Sequence: 1 MAQNLSCEWNLATEAILNKY.....REMLISKFRQYFKSLTSFRT 317

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1650	100.0	317	5	AAU74904	Aau74904 Amino aci
2	1238.5	75.1	330	6	ABP81696	Abp81696 Human pur
3	1238.5	75.1	334	3	AAB02842	Aab02842 Human G p
4	1238.5	75.1	334	3	AA71308	Aay71308 Human orp
5	1238.5	75.1	334	5	ABB90381	Abb90381 Human pol
6	1238.5	75.1	334	6	ABU92276	Abu92276 Human G p
7	1238.5	75.1	371	6	ABR41222	Abr41222 Human DIT
8	1238.5	75.1	379	5	AAE15633	Aae15633 Human G-p
9	1231.5	74.6	334	6	ABG72131	Abg72131 Human ade

10	1226.5	74.3	334	2	AAW19854	Aaw19854	Human	pur
11	1224.5	74.2	334	6	ABU63309	Abu63309	Human	ATP
12	1219.5	73.9	334	2	AAW22732	Aaw22732	Human	ATP
13	1216.5	73.7	387	4	AAU31029	Aau31029	Novel	hum
14	1185.5	71.8	335	7	ADC12680	Adc12680	Human	GPC
15	1014.5	61.5	258	3	AAB45376	Aab45376	Human	sec
16	479	29.0	373	5	ABP54317	Abp54317	Rat	P2Y p
17	479	29.0	373	6	ABU11903	Abu11903	Rat	purin
18	479	29.0	373	7	ADD46169	Add46169	Rat	Prote
19	474	28.7	373	4	AAE04389	Aae04389	Human	P2-
20	474	28.7	373	5	ABP54315	Abp54315	Bovine	P2
21	474	28.7	373	5	ABP54316	Abp54316	Human	P2Y
22	474	28.7	373	5	AAU10983	Aau10983	Purinergi	
23	474	28.7	373	5	AAU10984	Aau10984	Purinergi	
24	474	28.7	373	6	ABP81867	Abp81867	Human	pur
25	474	28.7	373	7	ADD46171	Add46171	Human	Pro
26	472.5	28.6	362	5	ABP54313	Abp54313	Chicken	P
27	472.5	28.6	362	5	ABP54314	Abp54314	Turkey	P2
28	472.5	28.6	362	6	ABU11901	Abu11901	Chicken	p
29	472.5	28.6	362	6	ABU11902	Abu11902	Turkey	pu
30	467	28.3	373	5	AAU10985	Aau10985	Purinergi	
31	426	25.8	330	7	ADC12674	Adc12674	Human	GPC
32	426	25.8	337	4	AAU04375	Aau04375	Human	G-p
33	426	25.8	337	5	AAE16171	Aae16171	Human	G-p
34	426	25.8	337	5	ABG76871	Abg76871	Human	G-p
35	426	25.8	337	5	ABB83819	Abb83819	Human	P2Y
36	426	25.8	337	5	ABG70271	Abg70271	Human	Pur
37	426	25.8	337	5	AAO14027	Aao14027	Human	pur
38	426	25.8	337	5	AAU77600	Aau77600	Human	P2Y
39	426	25.8	337	5	AAE21803	Aae21803	Human	AXO
40	426	25.8	337	5	ABP95602	Abp95602	Human	GPC
41	426	25.8	337	5	AAO15399	Aao15399	Human	G p
42	426	25.8	337	5	ABB79438	Abb79438	Human	P2Y
43	426	25.8	337	5	ABB81902	Abb81902	Human	G-p
44	426	25.8	337	5	ABG70287	Abg70287	Human	nov
45	426	25.8	337	6	ABP71377	Abp71377	Human	TGR

ALIGNMENTS

RESULT 1

AAU74904

ID AAU74904 standard; protein; 317 AA.

XX

AC AAU74904;

XX

DT 09-APR-2002 (first entry)

XX

DE Amino acid sequence of mouse G-protein coupled receptor TGR18 protein.

XX

KW Mouse; G-protein coupled; receptor; GPCR; TGR18; kidney disease;

KW signal transduction modulator; cerebral cavernous malformation;

KW hyperlipidemia; obesity; dyslexia; cardiac myxoma; renal failure;

KW nephritis; hypertension; liver disease; cirrhosis; blood disorder;

KW spleen-associated disorder; immune disorder.

XX

Db 61 LSISDFAFLCTLPLILIKSYANDKGTYGDLVCISNRYVLHTNLYTSILFLTTFISMDRYLLM 120
 Qy 121 KYPFREHFLOKKEFAILISLAVWALVTLEVLPMPLTFINSVPKEEGSNCIDYASSGNPEHN 180
 Db 121 KYPFREHFLOKKEFAILISLAVWALVTLEVLPMPLTFINSVPKEEGSNCIDYASSGNPEHN 180
 Qy 181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFVKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
 Db 181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFVKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
 Qy 241 FTPYHIMRNLRIASRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREM 300
 Db 241 FTPYHIMRNLRIASRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREM 300
 Qy 301 LISKFRQYFKSLTSFRT 317
 Db 301 LISKFRQYFKSLTSFRT 317

RESULT 2

ABP81696

ID ABP81696 standard; protein; 330 AA.

XX

AC ABP81696;

XX

DT 04-MAR-2003 (first entry)

XX

DE Human purinergic receptor P2U2 protein SEQ ID NO:567.

XX

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;

KW G protein-coupled receptor modulator; antibody; immune-related disease;

KW growth-related disease; cell regeneration-related disease; AIDS; cancer;

KW immunological-related cell proliferative disease; autoimmune disease;

KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;

KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;

KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;

KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;

KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;

KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;

KW ulcer.

XX

OS Homo sapiens.

XX

PN WO200261087-A2.

XX

PD 08-AUG-2002.

XX

PF 19-DEC-2001; 2001WO-US050107.

XX

PR 19-DEC-2000; 2000US-0257144P.

XX

PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX

PI Burmer GC, Roush CL, Brown JP;

XX

DR WPI; 2003-046718/04.

DR N-PSDB; ABZ42542.

XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX
PS Disclosure; Fig 1; 523pp; English.
XX
CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 330 AA;

Query Match 75.1%; Score 1238.5; DB 6; Length 330;
Best Local Similarity 72.2%; Pred. No. 3.3e-117;
Matches 228; Conservative 42; Mismatches 45; Indels 1; Gaps 1;

Qy 1 MAQNLSCEWLATEAILNKYYLSAFYAIEFIFGLLGNTVVFGYLFCKMKNWNSSNVYLFN 60
|| | :|:|||| || | ||||| || |||: |:||| ||:||:| :||||||:||||
Db 1 MAWNATCKNWLAAEALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 60
Qy 61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDDRYLLM 120
||:|| |||||:||:|||| ||||| ||||| ||||| |||||:||||:|
Db 61 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 120
Qy 121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHN 180
||||| |||||:||||:| ||||:||:| || | : |: | |:||||:| :|
Db 121 KYPFREHLLQKKEFAILISLAIWVLVLTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 180
Qy 181 LIYSLCLTLLGFLIPLSVMCFYYKMKVFLKRRSQQATALPLDKPQRLVVLAVVIFSIL 240
|||:||||||| |||||: ||||:|:| |||||:| |||||:| |||||:|
Db 181 LIYSMCLTLLGFLIPLFVMCFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSIL 240
Qy 241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299

Db 241 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 300
 Qy 300 MLISKFRQYFKSLTSF 315
 Db 301 MLMNQLRHNFKSLTSF 316

RESULT 3

AAB02842

ID AAB02842 standard; protein; 334 AA.
 XX
 AC AAB02842;
 XX
 DT 22-AUG-2000 (first entry)
 XX
 DE Human G protein coupled receptor hCHN10 protein SEQ ID NO:38.
 XX
 KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
 KW identification; agonist; screening; therapeutic; pharmaceutical; mutant.
 XX
 OS Homo sapiens.
 XX
 PN WO200022131-A2.
 XX
 PD 20-APR-2000.
 XX
 PF 13-OCT-1999; 99WO-US024065.
 XX
 PR 13-OCT-1998; 98US-00170496.
 PR 12-NOV-1998; 98US-0108029P.
 PR 20-NOV-1998; 98US-0109213P.
 PR 27-NOV-1998; 98US-0110060P.
 PR 16-FEB-1999; 99US-0120416P.
 PR 26-FEB-1999; 99US-0121852P.
 PR 12-MAR-1999; 99US-0123944P.
 PR 12-MAR-1999; 99US-0123945P.
 PR 12-MAR-1999; 99US-0123946P.
 PR 12-MAR-1999; 99US-0123948P.
 PR 12-MAR-1999; 99US-0123949P.
 PR 12-MAR-1999; 99US-0123951P.
 PR 28-MAY-1999; 99US-0136436P.
 PR 28-MAY-1999; 99US-0136437P.
 PR 28-MAY-1999; 99US-0136439P.
 PR 28-MAY-1999; 99US-0137127P.
 PR 28-MAY-1999; 99US-0137131P.
 PR 28-MAY-1999; 99US-0137567P.
 PR 29-JUN-1999; 99US-0141448P.
 PR 27-AUG-1999; 99US-0151114P.
 PR 03-SEP-1999; 99US-0152524P.
 PR 29-SEP-1999; 99US-0156555P.
 PR 29-SEP-1999; 99US-0156633P.
 PR 29-SEP-1999; 99US-0156634P.
 PR 29-SEP-1999; 99US-0156653P.
 PR 01-OCT-1999; 99US-0157280P.
 PR 01-OCT-1999; 99US-0157281P.
 PR 01-OCT-1999; 99US-0157282P.

XX

XX

XX

DR

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XX

Qy	1	MAQNLSCEWLAATEAILNKYLLSAFYAIEFIFGLLGNTVVFGYLFCEMKNWNSSNVYLEN	60
Db	5	MAWNATCKNWLAAEAALKYYLSIFYGIEFVVGVLGNTIVVGYIFSLKNWNSSNIYLEN	64
Qy	61	LSISDFAFLCTLPLILIKSYANDKGTYGDLVCISNRYVLHTNLTYLSILFLTFISMDRYLLM	120
Db	65	LSVSDLAFLCTLPLMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII	124
Qy	121	KYPFREHFLQKKEFAILISLAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHN	180
Db	125	KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN	184
Qy	181	LIYSLCLTLLGFLIPLSVMCFFYYKMVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL	240
Db	185	LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSIL	244
Qy	241	FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE	299
Db	245	FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLGDFHFRD	304
Qy	300	MLISKFRQYFKSLTSF	315
Db	305	MLMNQLRHNEFKSLTSF	320

RESULT 4

AAY71308

ID AAY71308 standard; protein; 334 AA.

XX

AC AAY71308;

XX

DT 02-NOV-2000 (first entry)

XX

DE Human orphan G protein-coupled receptor hCHN10.

XX

KW Human; orphan G protein-coupled receptor; GPCR; hCHN10; drug screening;
transmembrane receptor; expressed sequence tag; EST; signal cascade.

XX

OS Homo sapiens.

XX

PN WO200031258-A2.

XX

PD 02-JUN-2000.

XX

PF 13-OCT-1999; 99WO-US023687.

XX

PR 20-NOV-1998; 98US-0109213P.

PR 16-FEB-1999; 99US-0120416P.

PR 26-FEB-1999; 99US-0121852P.

PR 12-MAR-1999; 99US-0123946P.

PR 12-MAR-1999; 99US-0123949P.

PR 28-MAY-1999; 99US-0136436P.

PR 28-MAY-1999; 99US-0136437P.

PR 28-MAY-1999; 99US-0136439P.

PR 28-MAY-1999; 99US-0136567P.

PR 28-MAY-1999; 99US-0137127P.

PR 28-MAY-1999; 99US-0137131P.

PR 29-JUN-1999; 99US-0141448P.

PR 29-SEP-1999; 99US-0156555P.

PR 29-SEP-1999; 99US-0156633P.

PR 29-SEP-1999; 99US-0156634P.

PR 29-SEP-1999; 99US-0156653P.

PR 01-OCT-1999; 99US-0157280P.

PR 01-OCT-1999; 99US-0157281P.

PR 01-OCT-1999; 99US-0157282P.

PR 01-OCT-1999; 99US-0157293P.

PR 01-OCT-1999; 99US-0157294P.

PR 12-OCT-1999; 99US-00416760.

PR 12-OCT-1999; 99US-00417044.

XX

PA (AREN-) ARENA PHARM INC.

XX

PI Chen R, Dang HT, Liaw CW, Lin I;

XX

DR WPI; 2000-400068/34.

DR N-PSDB; AAD01135.

XX

PT Novel human orphan G protein-coupled receptors and the encoding cDNAs for
PT use in the identification of G protein-coupled receptor agonists.

XX

PS Claim 70; Page 87-88; 102pp; English.

XX

CC The present amino acid sequence is the hCHN10, an endogenous human orphan
CC G protein-coupled receptor (GPCR), expressed in kidney and thyroid. The
CC hCHN10 cDNA was identified using the human EST (expressed sequence tag)
CC 1365839 as a probe. The orphan GPCR of the invention, like all GPCRs has
CC seven transmembrane alpha helices with an extracellular N-terminus and an
CC intracellular C-terminus. However, no endogenous ligands has yet been
CC identified for the proteins of the invention. The orphan GPCRs may be
CC used in the identification of their endogenous ligands, and to screen
CC potential GPCR agonists and antagonists for use as pharmaceutical agents.
CC The proteins may also be used in the study of GPCR-mediated signalling
CC cascades, and to elucidate their precise role in normal and diseased
CC human conditions. Nucleic acid encoding human orphan GPCRs may be used
CC for tissue localisation expression analysis to provide information about
CC their function in healthy and pathological states

XX

SQ Sequence 334 AA;

Query Match 75.1%; Score 1238.5; DB 3; Length 334;
Best Local Similarity 72.2%; Pred. No. 3.4e-117;
Matches 228; Conservative 42; Mismatches 45; Indels 1; Gaps 1;

Qy	1	MAQNLS	CENWL	ATEAIL	NKYYLS	AFYAIE	FIFGL	LGNTV	VVFGY	LCMK	NWNSS	NVYLE	N	60				
			:				:		:		:							
Db	5	MAWNAT	CKNWL	AEEAA	EKKYLS	SIFYGI	EFVVG	VLGNT	IVVGY	IFSL	KNWNSS	NIYLE	N	64				
Qy	61	LSISDF	AF	LCTLP	ILIKSY	ANDKGT	YGDV	LCISN	RYVL	HTNL	YTSIL	FLTF	ISMD	RYLLM	120			
			:															
Db	65	LSVSD	LAFL	CTLP	MLIR	SYANG	NWIY	GDV	LCISN	RYVL	HANLY	TSIL	FLTF	ISID	RYLII	124		
Qy	121	KYPFRE	HFLQ	KKEFA	ILISL	AVWAL	VTLE	VLPM	LTFIN	SVPK	EEG	SNCID	YASS	GNPE	HN	180		
Db	125	KYPFRE	HLLQ	KKEFA	ILISL	AIWVL	VTLE	LLPIL	PLIN	PVIT	DNGT	TCND	FASS	GD	PNYN	184		
Qy	181	LIYSL	CLTL	LLGFL	IPLSV	MCFFY	YKMV	FLKRR	SQQQA	TALPL	DKPQ	RLVV	LAVV	IF	SIL	240		
Db	185	LIYSM	CLTL	LLGFL	IPLE	VMCF	FFYK	IALFL	KQRNR	QVATA	LPLE	KPLN	LVI	MAV	VIFSV	L	244	
Qy	241	FTPYH	IMRNL	RIAS	RLD	SWPQ	-GCT	QKA	IKSI	YTL	TRPL	AFLN	SAIN	PIFY	FLMG	DHYRE	299	
Db	245	FTPYH	VMRNV	RIAS	RLG	SWKQ	YQCT	QVV	INSF	YIV	TRPL	AFLN	SVIN	PV	FYFL	LGDH	FRD	304
Qy	300	MLISK	FRQY	FKSL	TSF													315
			:															
Db	305	MLMQ	LRHN	FKSL	TSF													320

RESULT 5

ABB90381

ID ABB90381 standard; protein; 334 AA.

XX

AC ABB90381;

XX

DT 24-MAY-2002 (first entry)

XX

DE Human polypeptide SEQ ID NO 2757.

XX
 KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
 KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200190304-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 18-MAY-2001; 2001WO-US016450.
 XX
 PR 19-MAY-2000; 2000US-0205515P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Birse CE, Rosen CA;
 XX
 DR WPI; 2002-122018/16.
 DR N-PSDB; ABL90790.
 XX
 PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 PT prevention of neural, immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 PT disorders.
 XX
 PS Claim 11; SEQ ID NO 2757; 2081pp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (ABL89449-ABL90853) and proteins
 CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 334 AA;

Query Match 75.1%; Score 1238.5; DB 5; Length 334;
 Best Local Similarity 72.2%; Pred. No. 3.4e-117;
 Matches 228; Conservative 42; Mismatches 45; Indels 1; Gaps 1;

Qy 1 MAQNLSCEWNLATEAILNKYYLSAFYAIEFIFGLLGNTVVFGYLFCKMKNWNSSNVYLFN 60
 || | :|:|||| || | ||||| || |||: |:||| ||:|:|:| :|:|:|:|:|:|:|

Db	5	MAWNATCKNWLAEEAALEKYYSIFYGIEFVVGVGLGNTIVVYGYIFSLKNWNSSNIYLFN	64
Qy	61	LSISDFAFLCTLPLILIKSYANDKGTYGDLVCISNRYVLHTNLYSILFLTFISMDRYLLM	120
Db	65	LSVSDLAFLCTLPLMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII	124
Qy	121	KYPFREHFLQKKEFAILISLAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHN	180
Db	125	KYPFREHLLQKKEFAILISLAIWVLVLTLELLPILPLINPVITDNGTTCNDFASSGDPNYN	184
Qy	181	LIYSLCLTLLGFLIPLSVMCFFYYKMVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL	240
Db	185	LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSIL	244
Qy	241	FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE	299
Db	245	FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD	304
Qy	300	MLISKFRQYFKSLTSF	315
Db	305	MLMNQLRHNFKSLTSF	320

RESULT 6

ID ABU92276 standard; protein; 334 AA.

AC ABU92276;

DT 16-JUL-2003 (first entry)

DE Human G protein-coupled receptor hCHN10.

KW Human; receptor; orphan G protein-coupled receptor; GPCR; hARE-3; hARE-4;

KW hARE-5; hRUP3; hRUP5; hRUP6; hRUP7; hGPCRZ7; hARE-1; hARE-2; hPPR1; hG2A;

KW hCHN3; hCHN4; hCHN6; hCHN8; hCHN9; hCHN10; hRUF4; signalling cascade.

OS Homo sapiens.

PN US2003017528-A1.

PD 23-JAN-2003.

PF 06-JUN-2001; 2001US-00875076.

PR 20-NOV-1998; 98US-0109213P.

PR 26-FEB-1999; 99US-0121852P.

PR 12-MAR-1999; 99US-0123949P.

PR 28-MAY-1999; 99US-0136437P.

PR 28-MAY-1999; 99US-0136567P.

PR 28-MAY-1999; 99US-0137131P.

PR 28-SEP-1999; 99US-0156333P.
PR 29-SEP-1999; 99US-0156555P.
PR 29-SEP-1999; 99US-0156634P.
PR 12-OCT-1999; 99US-00417044.

PA (CHEN/) CHEN R.
PA (DANG/) DANG H T.
PA (LIAW/) LIAW C W.
PA (LINI/) LIN I.

PI Chen R, Dang HT, Liaw CW, Lin I;

DR WPI; 2003-428952/40.

PT Novel endogenous, orphan, human G protein-coupled receptors useful for
PT identification of modulators of the receptor and as research tools for
PT understanding the role of the receptor in human body.

PS Claim 70; Page 41-42; 54pp; English.

The invention relates to a human G protein-coupled receptor (GPCR) appearing as ABU92259-ABU92277 (encoded by cDNAs ACA93256-ACA93274) named hARE-3, hARE-4, hARE-5, hRUP3, hRUP5, hRUP6, hRUP7, hGPCRZ7, hARE-1, hARE-2, hPPR1, hG2A, hCHN3, hCHN4, hCHN6, hCHN8, hCHN9, hCHN10 and hRUF4. Also included are a plasmid comprising a vector and one of the cDNAs above and a host cell comprising the plasmid. The GPCRs are useful for the direct identification of candidate compounds as inverse agonists, agonists or partial agonists. In vitro and in vivo systems incorporating GPCRs is useful for elucidating and understanding the roles these receptors play in the human condition, both normal and diseased, as well as understanding the role of constitutive activation as it applies to understanding the signalling cascade. The cDNAs are useful for making a probe for dot-blot analysis against tissue mRNA and/or RT-PCR identification of the expression of the receptor in tissue samples. The present sequence represents a GPCR of the invention

SQ Sequence 334 AA;

Query Match 75.1%; Score 1238.5; DB 6; Length 334;
Best Local Similarity 72.2%; Pred. No. 3.4e-117;
Matches 228; Conservative 42; Mismatches 45; Indels 1; Gaps 1;

QY 1 MAQNLSCEINWLATEAILNKYYLSAFYAIEFIFGLLGNTVVFGYLFCMKNWNSSNVYLFN 60
||| :||| || | |||| || ||| : ||| ||| :||| : ||| : |||
Db 5 MAWNATCKNLAAEALEKYYLSIFYGIEFVVGVLGNTIVVGYIFSLKNWNSSNIYLFN 64

```
Qy      61 LSISDFAFLCTLPLIKSYANDKGYGDVLCISNRYVLHTNLYSILFLT FISM DRYLLM 120
        ||:|| |||||:||:||| | ||||| ||||| |||||:|||:||::
Db      65 LSVSDLAFLCTLPLMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLT FISIDRYLII 124
```

```
Qy      121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHN 180
        ||||| |||||:| |||:|:| || | : |:| |:|:| :|
Db      125 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 184
```

Qy 181 LIYSLCLTLLGFLIPLSVMCFFYYKMOVFLKRRSQQATALPLDKPQRLVVLAVVIFSIL 240
|||:||||||| |||||: |||:|: |||||:| ||:|||||:

Db 185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL 244

Qy 241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
 |||||:||||:||||| || | ||| | | | :||||||| |||:||||:||||:|

Db 245 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFVFYFLLGDHFRD 304

Qy 300 MLISKFRQYFKSLTSF 315
 ||::: | |||||

Db 305 MLMNQLRHNFKSLTSF 320

RESULT 7

ABR41222

ID ABR41222 standard; protein; 371 AA.

XX

AC ABR41222;

XX

DT 02-JUN-2003 (first entry)

XX

DE Human DITHP receptor.

XX

KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;

KW cancer; cell proliferative disorder; autoimmune disorder;

KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;

KW neurological disorder; gastrointestinal disorder; transport disorder;

KW connective tissue disorder; drug screening; proteome analysis;

KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;

KW disease model; toxicological testing; transcript imaging; receptor.

XX

OS Homo sapiens.

XX

PN WO200297031-A2.

XX

PD 05-DEC-2002.

XX

PF 27-MAR-2002; 2002WO-US010056.

XX

PR 28-MAR-2001; 2001US-0279619P.

PR 29-MAR-2001; 2001US-0280067P.

PR 29-MAR-2001; 2001US-0280068P.

PR 16-MAY-2001; 2001US-0291280P.

PR 17-MAY-2001; 2001US-0291829P.

PR 17-MAY-2001; 2001US-0291849P.

PR 19-JUN-2001; 2001US-0299428P.

PR 20-JUN-2001; 2001US-0299776P.

PR 20-JUN-2001; 2001US-0300001P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;

PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;

PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;

PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;

PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;

XX

DR WPI; 2003-129518/12.

DR N-PSDB; ACC46165.

XX
PT Novel human diagnostic and therapeutic polypeptide useful for identifying
PT test compound which specifically binds to a polypeptide encoded by human
PT diagnostic and therapeutic polynucleotide, and to induce antibodies.
XX
PS Claim 27; SEQ ID NO 757; 591pp; English.
XX
CC The invention relates to novel human diagnostic and therapeutic
CC polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded
CC proteins (DITHP; ABR41136-ABR41812). The invention also relates to
CC polynucleotide sequences at least 90% identical to the dithp cDNA
CC sequences of the invention; recombinant vectors, host cells and
CC transgenic organisms comprising a dithp nucleic acid sequence; the
CC recombinant production of DITHP proteins; antibodies specific for DITHP
CC proteins; microarrays comprising dithp nucleic acid sequences; methods of
CC detecting dithp nucleotide and protein sequences; methods of screening
CC for compounds which specifically bind a DITHP protein; and methods of
CC assessing the toxicity of test compounds using a dithp hybridisation
CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
CC diagnosis of a wide variety of conditions including cancer and other cell
CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
CC viral, fungal or parasitic infections; hormonal disorders; metabolic
CC disorders; neurological disorders; gastrointestinal disorders; transport
CC disorders; and connective tissue disorders. They may also be used to
CC screen for modulators of protein activity or gene expression. DITHP
CC proteins can additionally be used in analysis of the proteome of a tissue
CC or cell type and to induce antibodies. The dithp nucleic acids are
CC additionally useful in somatic or germline gene therapy of the disorders
CC mentioned above, as a source of antisense sequences, as a source of
CC probes and primers, in genotyping and identification of individuals, in
CC the generation of transgenic animal models of human disease or knock in
CC humanised animals, in toxicological testing, and in transcript imaging.
CC The present sequence represents a DITHP protein which has receptor
CC activity. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 371 AA;

Query Match 75.1%; Score 1238.5; DB 6; Length 371;
Best Local Similarity 72.2%; Pred. No. 3.9e-117;
Matches 228; Conservative 42; Mismatches 45; Indels 1; Gaps 1;

QY 1 MAQNLSCEWNLATEAILNKYYLSAFYAIEFIFGLLGNTVVVFGYLFCKMKNWNSSNVYLFN 60
|| | :|:|||| || | |||| || |||: |:||| ||:||:| :|||||||:||||
Db 42 MAWNATCKNWLAAEAALAKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 101
QY 61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDDRYLLM 120
||:|| |||||:|:|||| ||||| ||||| |||||:||||:|
Db 102 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 161
QY 121 KYPFREHFLQKKEFAILISLAWVALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHN 180
|||||| |||||:|||||:| ||||:|:| || | : |:| |:||||:| :|
Db 162 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 221
QY 181 LIYSLCLTLLGFLIPLSVMCFYYKMMVFLKRRSQQAATAPLDKPPQLVVLAVVIFSIL 240
||||:||||||| |||||: |:|:|:| |||||:| ||:|:||||:|

Db 222 LIYSMCLTLLGFLIPLFVMCFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL 281

Qy 241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
 |||||:||||:||||| || | ||| | | | :||||||| |||:||||:||||:|

Db 282 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 341

Qy 300 MLISKFRQYFKSLTSF 315
 ||::: | |||||

Db 342 MLMNQLRHNFKSLTSF 357

RESULT 8

AAE15633

ID AAE15633 standard; protein; 379 AA.

XX

AC AAE15633;

XX

DT 12-MAR-2002 (first entry)

XX

DE Human G-protein coupled receptor-3 (GCREC-3) protein.

XX

KW Human; G-protein coupled receptor-3; GCREC-3; therapy; cancer; stroke;
 KW cell proliferative disorder; neurological; epilepsy; Parkinson's disease;
 KW Alzheimer's disease; inflammation; thyroiditis; haemolytic anaemia; AIDS;
 KW Acquired Immune Deficiency Syndrome; dementia; nootropic; cholelithiasis;
 KW multiple sclerosis; atherosclerosis; angina pectoris; gastroenteritis;
 KW diabetes; ulcer; viral infection; immunosuppressive.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	Domain	187. .206
FT		/label= Transmembrane_domain
FT	Domain	234. .253
FT		/label= Transmembrane_domain
FT	Domain	276. .296
FT		/label= Transmembrane_domain
FT	Domain	319. .342
FT		/label= Transmembrane_domain

XX

PN WO200198351-A2.

XX

PD 27-DEC-2001.

XX

PF 15-JUN-2001; 2001WO-US019275.

XX

PR 16-JUN-2000; 2000US-0212483P.

PR 22-JUN-2000; 2000US-0213954P.

PR 29-JUN-2000; 2000US-0215209P.

PR 07-JUL-2000; 2000US-0216595P.

PR 14-JUL-2000; 2000US-0218936P.

PR 19-JUL-2000; 2000US-0219154P.

PR 21-JUL-2000; 2000US-0220141P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Lal P, Baughn MR, Hafalia AJA, Nguyen DB, Gandhi AR, Kallick DA;

PI Griffin JA, Yue H, Khan FA, Patterson C, Lu DAM, Tribouley CM;
PI Lu Y, Walia NK, Graul R, Yao MG, Yang J, Ramkumar J, Au-Young J;
PI Elliott VS, Hernandez R, Walsh RT, Borowsky ML, Thornton M, He A;
XX
DR WPI; 2002-075627/10.
DR N-PSDB; AAD24958.

XX
PT Isolated human G-protein coupled receptor polypeptides and the use of
PT these sequences in the diagnosis, treatment and prevention of diseases
PT and in the assessment of exogenous compounds on the expression of the
PT receptors.

XX
PS Claim 1; Page 115-116; 143pp; English.
XX

CC The invention relates to isolated human G-protein coupled receptor
CC (GCREC) polypeptides and their biologically active fragments. GCREC and
CC protein is useful in treating a disease or condition associated with an
CC increase or decrease in expression of functional GCREC. The GCREC's are
CC useful in the diagnosis, treatment and prevention of cell proliferative
CC disorders (cancer, leukaemia, melanoma); neurological disorders (stroke,
CC epilepsy, Parkinson's disease, dementia, Alzheimer's disease); autoimmune
CC inflammatory disorder (thyroiditis, haemolytic anaemia, AIDS, multiple
CC sclerosis); cardiovascular disorder (atherosclerosis, angina pectoris),
CC gastrointestinal disorder (ulcer, cholelithiasis, gastroenteritis),
CC metabolic disorders (diabetes); viral infections (herpes virus) and in
CC the assessment of the effects of exogenous compounds on the expression of
CC the nucleic acid and amino acid sequences. The present sequence is human
CC GCREC-3 protein

XX
SQ Sequence 379 AA;

Query Match 75.1%; Score 1238.5; DB 5; Length 379;
Best Local Similarity 72.2%; Pred. No. 4e-117;
Matches 228; Conservative 42; Mismatches 45; Indels 1; Gaps 1;

Qy 1 MAQNLSCEWNLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCKMKNWNSSNVYLFN 60
|| | :|:|||| || | |||| || |||: |:|| | |:|:| :|||||:||||
Db 50 MAWNATCKNWLAAEALEKYYLSIFYGIEFVVGVLGNTIVVGYIFSLKNWNSSNIYLFN 109

Qy 61 LSISDFAFLCTLPILIKSYANDKGTYGDLVCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
||:|| |||||:|:|||| | ||||| ||||| |||||:|:|:|:
Db 110 LSVSDLAFCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 169

Qy 121 KYPFREHFLQKKEFAILISLAWLVTLEVLPMPLTFINSVPKEEGSNCIDYASSGNPEHN 180
||||| |||||:|:| ||||:|:| || | : |: | |:|:|:| :|
Db 170 KYPFREHLLQKKEFAILISLAIWVLVTLELLPLPLINPVITDNGTTCNDFASSGDPNYN 229

Qy 181 LIYSLCLTLLGFLIPLSVMCFYYKMWVFLKRRSQQQATAPLDKPQRLVVLAVVIFSIL 240
|||:|:|:|:|:| |||||:|:|:|:|:| |||||:| ||:|:|:|:|:
Db 230 LIYSMCLTLLGFLIPLFVMCFYYKIALFLKQRNRQVATAPLEKPLNLVIMAVVIFSIL 289

Qy 241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
|||:|:|:|:| || | || | || | :|:|:|:| ||:|:|:|:|:|:
Db 290 FTPYHVMRNVRIASRLGSKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLGDFHFRD 349

Qy 300 MLISKFRQYFKSLTSF 315
||::: | |||||

RESULT 9

ABG72131

ID ABG72131 standard; protein; 334 AA.

XX

AC ABG72131;

XX

DT 30-JAN-2003 (first entry)

XX

DE Human adenosine receptor.

XX

KW Human; mammalian; adenosine receptor; G-protein coupled receptor; GPCR;
 KW adenosine-mediated medical condition; vasodilation; hypotension;
 KW reversal of tachycardia; chronic renal disease; thyroid disorder;
 KW inflammation; asthma; hypertensive; antiarrhythmic; antiinflammatory;
 KW receptor.

XX

OS Homo sapiens.

XX

PN US2002137887-A1.

XX

PD 26-SEP-2002.

XX

PF 17-JAN-2001; 2001US-00765034.

XX

PR 17-JAN-2001; 2001US-00765034.

XX

PA (HEDR/) HEDRICK J A.

PA (LACH/) LACHOWICZ J E.

PA (WANG/) WANG W.

PA (GUST/) GUSTAFSON E L.

XX

PI Hedrick JA, Lachowicz JE, Wang W, Gustafson EL;

XX

DR WPI; 2003-074992/07.

DR N-PSDB; ABS57291.

XX

PT Novel isolated mammalian adenosine receptor polypeptide useful for
 PT identifying an agonist or antagonist of the receptor for treating
 PT vasodilation, hypotension, chronic renal diseases, thyroid disorders and
 PT inflammation.

XX

PS Claim 2; Page 16-17; 19pp; English.

XX

CC The present invention relates to the isolation of a mammalian (human)
 CC adenosine receptor, and the polynucleotide sequence encoding it. The
 CC cloned receptor resembles a member of the G-protein coupled receptor
 CC (GPCR) superfamily that contains 7-transmembrane domains. The adenosine
 CC receptor is useful for identifying agonists and antagonists of the
 CC receptor, which may be useful for treating an adenosine-mediated medical
 CC condition. The adenosine receptor polypeptide sequence is also useful as
 CC an antigen to elicit antibody production in an immunologically competent
 CC host. An antibody which binds specifically to the adenosine receptor is
 CC useful for treating medical conditions caused or mediated by adenosine
 CC such as vasodilation, hypotension, reversal of tachycardia, chronic renal

CC diseases, thyroid disorders and inflammation (e.g. asthma). The antibody
 CC can also be used to purify the adenosine receptor, or as a basis for
 CC immunoassays of the receptor. The polynucleotide sequence encoding the
 CC adenosine receptor is useful for producing vectors and host cells
 CC containing the vectors. It is also useful for measuring expression of a
 CC mammalian adenosine receptor gene in a biological sample. The present
 CC sequence represents human adenosine receptor
 XX

SQ Sequence 334 AA;

Query Match 74.6%; Score 1231.5; DB 6; Length 334;
 Best Local Similarity 71.8%; Pred. No. 1.8e-116;
 Matches 227; Conservative 42; Mismatches 46; Indels 1; Gaps 1;

Qy	1	MAQNLS	CENWL	ATEAIL	NKYYS	SAFYA	IEFIF	GLLGN	VTVV	FGYLF	CMKNW	NSSNV	YLFN	60
			:					:		:				
Db	5	MAWNAT	CKNWL	AEEAA	LEKYY	LSIFY	GIEFV	VGVLG	NTIV	VYGYI	FSLKN	WNSSN	IYLFN	64
Qy	61	LSISD	FAFLC	TLPLI	KSYAN	DKGT	YGDV	LCISN	RYVL	HTNL	YTSIL	FLTFI	SMDRY	LLM 120
		:		:	:									
Db	65	LSVSD	LAFLC	TLPLM	LIRSY	ANGN	WIYGD	VLCIS	NRYV	LHAN	LYTSI	LFLTF	ISIDR	YLII 124
Qy	121	KYPFR	EHFLQ	KKEFA	ILISL	AVWAL	VTLE	VLPL	MFTFI	NSVP	KKEGS	NCIDY	ASSGN	PEHN 180
Db	125	KYPFR	EHLQK	KEFAI	LISLA	IWVL	VTLE	LLPIL	PLINP	VITDN	GTTCN	DFASS	GDPNY	N 184
Qy	181	LIYSL	CLTLL	GLFLI	PLSVM	CFYYK	MVFL	KRRS	QQQAT	ALPLD	KPQRL	VVLAV	VIFSIL	240
		:												
Db	185	LIYSM	CLTLL	GLFLI	PLFVM	CFYYK	IALFL	KQRNR	QVATA	LPLEK	PLNLV	IMAVV	IFSVP	244
Qy	241	FTPYH	IMRNL	RIASR	LDSPQ	-GCTQ	KAIKS	IYTL	TRPLA	FLNSA	INPIF	YFLMG	DHYRE	299
		:												
Db	245	FTPYH	VMRNV	RIASR	LGSKQ	YQCTQ	VVINS	FYIV	TRPLA	FLNSV	INPVF	YFLLG	DHFRD	304
Qy	300	MLISK	FRQYF	KSLTS	F 315									
		:												
Db	305	MLMNQ	LRHNF	KSLTS	F 320									

RESULT 10

AAW19854

ID AAW19854 standard; protein; 334 AA.

XX

AC AAW19854;

XX

DT 11-SEP-1997 (first entry)

XX

DE Human purinergic receptor P2U2.

XX

KW P2U2 receptor; purinergic receptor; diagnosis; therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 1. .23

FT /label= N-terminal_domain

FT Domain 24. .49

```

FT          /label= TMI
FT          /note= "transmembrane domain I"
FT  Domain  50. .60
FT          /label= ICDI
FT          /note= "intracellular domain I"
FT  Domain  61. .82
FT          /label= TMII
FT          /note= "transmembrane domain II"
FT  Domain  83. .99
FT          /label= ECDI
FT          /note= "extracellular domain I"
FT  Domain  100. .119
FT          /label= TMIII
FT          /note= "transmembrane domain III"
FT  Domain  120. .141
FT          /label= ICDII
FT          /note= "intracellular domain II"
FT  Domain  142. .161
FT          /label= TMDIV
FT          /note= "transmembrane domain IV"
FT  Domain  162. .183
FT          /label= ECDII
FT          /note= "extracellular domain II"
FT  Domain  184. .207
FT          /label= TMDV
FT          /note= "transmembrane domain V"
FT  Domain  208. .233
FT          /label= ICDIII
FT          /note= "intracellular domain III"
FT  Domain  234. .256
FT          /label= TMDVI
FT          /note= "transmembrane domain VI"
FT  Domain  257. .276
FT          /label= ECDIII
FT          /note= "extracellular domain III"
FT  Domain  277. .300
FT          /label= TMDVII
FT          /note= "transmembrane domain VII"
FT  Domain  301. .334
FT          /label= C-terminal_domain
XX
PN  WO9720045-A2.
XX
PD  05-JUN-1997.
XX
PF  08-NOV-1996;   96WO-US018175.
XX
PR  15-NOV-1995;   95US-0006782P.
PR  15-NOV-1995;   95US-00559524.
XX
PA  (CORT-) COR THERAPEUTICS INC.
XX
PI  Conley PB,  Jantzen H;
XX
DR  WPI; 1997-310601/28.
DR  N-PSDB; AAT71900.
XX

```

PT New isolated purinergic receptor sub-type - used to develop products for
PT diagnosis and therapy, e.g. for screening for agonists and antagonists
PT which can modulate activation.
XX
PS Claim 1; Fig 1A-B; 36pp; English.
XX
CC P2U2 receptor (AAW19854) is a novel human purinergic receptor subtype
CC that is abundantly expressed in kidney and in many cell lines of
CC megakaryocytic or erythroleukaemic origin and which is activated by ATP,
CC UDP, UTP and UDP. Its amino acid sequence was deduced from a cDNA clone
CC derived from DAMI (ATCC CRL 9792) cells. P2U2 and its polypeptides can be
CC expressed in host cells and used to develop diagnostic and therapeutic
CC agents. Antagonists and agonists based on the extracellular domains of
CC P2U2 receptor, or which affect receptor function by binding to one of the
CC intracellular domains, can be used to treat diseases caused by aberrant
CC activation of this receptor or to treat diseases whose symptoms can be
CC ameliorated by stimulating or inhibiting the activity of the receptor
XX
SQ Sequence 334 AA;

Query Match 74.3%; Score 1226.5; DB 2; Length 334;
Best Local Similarity 71.5%; Pred. No. 5.7e-116;
Matches 226; Conservative 42; Mismatches 47; Indels 1; Gaps 1;

Qy	1	MAQNLSCEWNLATEAILNKYYLSAFYAIEFIFGLLGNTVTVVFGYLCMKNNWSSNVYLEN	60
		: : : : : : :	
Db	5	MAWNATCKNWLAEEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWSSNIYLEN	64
Qy	61	LSISDFAFLCTLPLIKSYANDKGTGVDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM	120
		: : : : :	
Db	65	LSVSDLAFLCTLPLMIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII	124
Qy	121	KYPFREHFLQKKEFAILISLAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHN	180
		: : : : :	
Db	125	KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN	184
Qy	181	LIYSLCLTLLGFLIPLSVMCFFYYKMVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL	240
		: : : : : : :	
Db	185	LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSIL	244
Qy	241	FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE	299
		: : : : : :	
Db	245	FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRALGFLNSVINPVFYFLLGDHFRD	304
Qy	300	MLISKFRQYFKSLTSF	315
		: :	
Db	305	MLMNQLRHNFKSLTSF	320

RESULT 11

ABU63309

ID ABU63309 standard; protein; 334 AA.

XX

AC ABU63309;

XX

DT 18-SEP-2003 (first entry)

XX

DE Human ATP receptor.
 XX
 KW Human; receptor; ATP receptor; G-protein coupled receptor; gene therapy;
 KW 7-transmembrane receptor; asthma; allergic rhinitis; hypertension; ulcer;
 KW angina pectoris; allergy; psychosis; depression; migraine; vomiting;
 KW benign prostatic hypertrophy; arterial thrombosis; myocardial infarction;
 KW urinary retention; angioplasty; cystic fibrosis; Parkinson's disease;
 KW acute heart failure; hypotension; thrombolysis; osteoporosis.
 XX
 OS Homo sapiens.
 XX
 PN US2003054487-A1.
 XX
 PD 20-MAR-2003.
 XX
 PF 16-OCT-2002; 2002US-00270587.
 XX
 PR 11-JAN-1996; 96US-0009902P.
 PR 10-JAN-1997; 97US-00781456.
 PR 20-JUL-2001; 2001US-00908593.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Li Y;
 XX
 DR WPI; 2003-540615/51.
 DR N-PSDB; ACD27619.
 XX
 PT New polynucleotide, useful for producing a medicament for treating
 PT asthma, allergic rhinitis or hypertension.
 XX
 PS Claim 1; Fig 1; 24pp; English.
 XX
 CC The invention relates to an isolated polynucleotide encoding a G-protein
 CC coupled, 7-transmembrane ATP receptor. The polynucleotide is useful for
 CC producing a medicament for treating asthma, allergic rhinitis or
 CC hypertension. Antagonists for the the ATP receptor can be used to treat
 CC angina pectoris, ulcers, allergies, psychoses, depression, migraine,
 CC vomiting, benign prostatic hypertrophy, arterial thrombosis, myocardial
 CC infarction, thrombolysis, angioplasty, cystic fibrosis. Agonists of the
 CC ATP receptor can be used to treat Parkinson's disease, acute heart
 CC failure, hypotension, urinary retention and osteoporosis. The present
 CC sequence represents the amino acid sequence of the human ATP receptor
 XX
 SQ Sequence 334 AA;

Query Match 74.2%; Score 1224.5; DB 6; Length 334;
 Best Local Similarity 71.5%; Pred. No. 9e-116;
 Matches 226; Conservative 43; Mismatches 46; Indels 1; Gaps 1;

QY 1 MAQNLSCEWNLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCKMKNWNSSNVYLEN 60
 || | :|:|||| || | ||||| || |||: |:||| ||:|||:| :|||||||:||||
 Db 5 MAWNATCKNWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLEN 64
 QY 61 LSISDFAFLCTLPILIKSYANDKGYTGDVLCISNRYVLHTNLYTSILFLTTFISMDRYLLM 120
 ||:|| |||||:|:|:|||| | ||||| ||||| ||||| |||||:||||:|
 Db 65 LSVSDLAFCLCTPLMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTTFISIDRYLII 124

Qy 121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKKEGSNCIDYASSGNPEHN 180
 ||||| ||||| |||||:| ||||:|:| || | : |: | |:| |||:| :|
 Db 125 KYPFREHLLQKKECAILISLAMWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 184

Qy 181 LIYSLCLTLLGFLIPLSVMCFFYYKMVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
 ||||:||||| |||||:| :|||:|:| |||||:| ||:| |||||:|
 Db 185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSIL 244

Qy 241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
 ||||:|:|:| || | || | | :||:| |||| | ||:| ||||:|:|:|
 Db 245 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPVAFLNSVINPVFYFLVGDHFRD 304

Qy 300 MLISKFRQYFKSLTSF 315
 ||::: | |||||
 Db 305 MLMNQLRHNFKSLTSF 320

RESULT 12

AAW22732

ID AAW22732 standard; protein; 334 AA.

XX

AC AAW22732;

XX

DT 07-OCT-1997 (first entry)

XX

DE Human ATP receptor.

XX

KW ATP receptor; G-protein coupled receptor; agonist; antagonist.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 212

FT /note= "encoded by TCC"

FT Misc-difference 235

FT /note= "encoded by TCG"

FT Misc-difference 244

FT /label= Unknown

FT /note= "encoded by CYT"

XX

PN WO9724929-A1.

XX

PD 17-JUL-1997.

XX

PF 11-JAN-1996; 96WO-US000392.

XX

PR 11-JAN-1996; 96WO-US000392.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Li Y;

XX

DR WPI; 1997-372505/34.

DR N-PSDB; AAT75146.

XX

PT Isolated human ATP receptor - agonists and antagonists of which are

PT useful in treatment of, e.g. asthma, hypertension, arterial thrombosis
PT and psychotic and neurological disorders.
XX
PS Claim 15; Fig 1A-C; 53pp; English.
XX
CC Human ATP receptor (AAW22732) is structurally related to the G protein-
CC coupled receptor family. It shows 29.8% identity to a murine P2u
CC receptor. Its amino acid sequence was deduced from a human placental cDNA
CC clone (AAT75146). Recombinant ATP receptor can be expressed in bacterial
CC (e.g. E. coli), mammalian (e.g. COS) or insect (e.g. Sf9) host cells and
CC used to screen for agonists and antagonists useful in the treatment of
CC conditions related to underexpression of the receptor (e.g. asthma,
CC Parkinson's disease, acute heart failure, hypotension, urinary retention
CC and osteoporosis) or underexpression of the receptor (e.g. arterial
CC thrombosis, hypertension, thrombolysis, angioplasty, cystic fibrosis,
CC ulcers, asthma, allergy, benign prostatic hypertrophy, psychotic and
CC neurological disorders, dyskinesias, endogenous anorexia and bulimia)
XX
SQ Sequence 334 AA;

Query Match 73.9%; Score 1219.5; DB 2; Length 334;
Best Local Similarity 71.2%; Pred. No. 2.9e-115;
Matches 225; Conservative 43; Mismatches 47; Indels 1; Gaps 1;

Qy	1	MAQNLSCEWLATEAILNKYYLSAFYAIEFIFGLLGNTVTVFGYLFCKMKNWNSSNVYLFN	60
		: : : : : :	
Db	5	MAWNATCKNWLAAEALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN	64
Qy	61	LSISDFAFLCTLPLIKSYANDKGTYGDLVCISNRYVLHTNLTYTSILFLTFISMDRYLLM	120
		: : : : :	
Db	65	LSVSDLAFLCTLPLMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII	124
Qy	121	KYPFREHFLQKKEFAILISLAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHN	180
		: : : : :	
Db	125	KYPFREHLLQKKECAILISLAMWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN	184
Qy	181	LIYSLCLTLLGFLIPLSVMCFFYYKMVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL	240
		: : : : : : :	
Db	185	LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSIX	244
Qy	241	FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE	299
		: : : : : :	
Db	245	FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPVAFLNSVINPVFYFLVGDHFRD	304
Qy	300	MLISKFRQYFKSLTSF	315
		: :	
Db	305	MLMNQLRHNFKSLTSF	320

RESULT 13

AAU31029

ID AAU31029 standard; protein; 387 AA.

XX

AC AAU31029;

XX

DT 18-DEC-2001 (first entry)

XX

DE Novel human secreted protein #1520.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US008656.
 XX
 PR 18-APR-2000; 2000US-00552929.
 PR 26-JAN-2001; 2001US-00770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-611725/70.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy.
 XX
 PS Claim 20; Page 392; 765pp; English.
 XX
 CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising the
 CC nucleic acids encoding the polypeptides and cells genetically engineered
 CC to express them are also useful for producing the proteins. The proteins
 CC are useful in genetic vaccination, testing and therapy, and can be used
 CC as nutritional supplements. They may be used to increase stem cell
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
 CC and/or nerve tissue growth or regeneration; immune suppression and/or
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
 CC AAU29510-AAU33304 represent the amino acid sequences of novel human
 CC secreted proteins of the invention
 XX
 SQ Sequence 387 AA;

Query Match 73.7%; Score 1216.5; DB 4; Length 387;
 Best Local Similarity 71.1%; Pred. No. 7.2e-115;
 Matches 224; Conservative 43; Mismatches 47; Indels 1; Gaps 1;

Qy 2 AQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNTVVFGYLFCKMKNWNSSNVYLENL 61
 | | :|:| | | | | | | | | | : | :| | | :| | | | :| | | | |
 Db 59 AWNATCKHWLAEEAALEKYYLSIFYGIEFVVGVLGNTIVVGYIFSLKNWNSSNIYLENL 118
 Qy 62 SISDFAFLCTLPILIKSYANDKGTYGVDVLCISNRYVLHTNLYTSILFLTFSMDRYLLMK 121

Db	119	SVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLIK	178
Qy	122	YPFREHFLQKKEFAILISLAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHNL	181
Db	179	YPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYNL	238
Qy	182	IYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSILF	241
Db	239	IYSMCLTLLGFSIPLFVMCLFYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSILF	298
Qy	242	TPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREM	300
Db	299	TPYHVMRNVRIASRLGSWKQYQCTQVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRDM	358
Qy	301	LISKFRQYFKSLTSF	315
Db	359	LMNQLRHNFKSLTSF	373

RESULT 14

ADC12680

ID ADC12680 standard; protein; 335 AA.

XX

AC ADC12680;

XX

DT 18-DEC-2003 (first entry)

XX

DE Human GPCR protein, SEQ ID No 12.

XX

KW G protein-coupled receptor; GPCR; antibacterial; fungicide; protozoacide;
 KW virucide; antirheumatic; antiarthritic; tranquiliser; antidiabetic;
 KW osteopathic; nootropic; neuroprotective; anorectic; cardiant;
 KW neuroleptic; cytostatic; antiparkinsonian; hypotensive; hypertensive;
 KW antiulcer; antiallergic; anticonvulsant; analgesic; infection;
 KW rheumatoid arthritis; chronic obstructive pulmonary diseases; COPD;
 KW asthma; non-insulin dependent diabetes; obesity; osteoporosis;
 KW Alzheimer's disease; age-related macular degeneration;
 KW myocardial infarction; schizophrenia; osteoarthritis; cancer;
 KW Parkinson's disease; congestive heart failure; hypotension; hypertension;
 KW ulcer; allergy; benign prostatic hyperplasia; seizure disorder; anxiety;
 KW obsessive compulsive disorder; Cushing's syndrome; hypopituitarism; pain;
 KW human.

XX

OS Homo sapiens.

XX

PN WO2003000893-A2.

XX

PD 03-JAN-2003.

XX

PF 24-JUN-2002; 2002WO-IB002357.

XX

PR 26-JUN-2001; 2001US-0301095P.

PR 06-NOV-2001; 2001US-0333185P.

XX

PA (DECO-) DECODE GENETICS EHF.

XX

Qy 195 PLSVMCFFYYKMVFLKRRSQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIAS 254
 || |||||: :||:|:| |||||:| ||:|||||:|||||:|:|:|
 Db 181 PLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVLFTPYHVMRNVRIAS 240
 Qy 255 RLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQYFKSLT 313
 || || | || | | :||||||| ||:||||:|:|:|:|:|:| | ||||
 Db 241 RLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRDMLNQLRHNFKSLT 300
 Qy 314 SF 315
 ||
 Db 301 SF 302

RESULT 15

AAB45376

ID AAB45376 standard; protein; 258 AA.
 XX
 AC AAB45376;
 XX
 DT 14-FEB-2001 (first entry)
 XX
 DE Human secreted protein sequence encoded by gene 37 SEQ ID NO:128.
 XX
 KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
 KW antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
 KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
 KW fungicide; ophthalmological; vulnerary; gene therapy; autoimmune disease;
 KW hyperproliferative disorder; cardiovascular disorder; angiogenesis;
 KW cerebrovascular disorder; nervous system disorder; infection; skin aging;
 KW ocular disorder; wound healing; food additive; preservative.
 XX
 OS Homo sapiens.
 XX
 PN WO200061628-A1.
 XX
 PD 19-OCT-2000.
 XX
 PF 06-APR-2000; 2000WO-US009070.
 XX
 PR 09-APR-1999; 99US-0128695P.
 PR 14-JAN-2000; 2000US-0176052P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM, Komatsoulis G;
 XX
 DR WPI; 2000-619228/59.
 XX
 PT New nucleic acid molecules encoding 49 human secreted proteins for
 PT diagnosing, preventing, treating or ameliorating medical conditions and
 PT used as food additives or preservatives.
 XX
 PS Disclosure; Page 447-448; 454pp; English.
 XX
 CC The polynucleotide sequences given in AAC81086 to AAC81134 encode the
 CC human secreted proteins given in AAB45308 to AAB45356. AAB45357 to

CC AAB45384 represent human secreted polypeptide sequences and proteins
 CC homologous to them, which are given in the exemplification of the present
 CC invention. Human secreted proteins have activities based on the tissues
 CC and cells the genes are expressed in. Examples of activities include:
 CC antiarthritic; immunosuppressive; antirheumatic; antiproliferative;
 CC cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
 CC neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
 CC and vulnerary. The polynucleotides and polypeptides can be used to
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
 CC in diagnosing a pathological condition or susceptibility to a
 CC pathological condition. Disorders which are diagnosed or treated include
 CC autoimmune diseases, hyperproliferative disorders, cardiovascular
 CC disorders, cerebrovascular disorders, angiogenesis, nervous system
 CC disorders, infections caused by bacteria, viruses and fungi and ocular
 CC disorders. The polypeptides can also be used to aid wound healing and
 CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
 CC maintain organs before transplantation, for supporting cell culture of
 CC primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content, lipid, protein,
 CC carbohydrate, vitamins, minerals, cofactors and other nutritional
 CC components. AAC81077 to AAC81085 and AAB45307 represent sequences used in
 CC the exemplification of the present invention
 XX
 SQ Sequence 258 AA;

Query Match 61.5%; Score 1014.5; DB 3; Length 258;
 Best Local Similarity 72.9%; Pred. No. 1.5e-94;
 Matches 188; Conservative 33; Mismatches 36; Indels 1; Gaps 1;

Qy	20	YYLSAFYAIEFIFGLLGNVTVVFGYLFCKMKNWNSSNVYLEFNLSISDFAFLCTLPILIKSY	79
		: : : : : : : : :	
Db	1	YYLSIFYGIEFVVGVLGNTIVVGYIFSLKNWNSSNIYLEFNLSVSDLAFLCTLPMLIRSY	60
Qy	80	ANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILIS	139
		: : :	
Db	61	ANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLIKYPFREHLLQKKEFAILIS	120
Qy	140	LAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLSVM	199
		: : : : : : : : : :	
Db	121	LAIWVLTLELLPILPLINPVITDNGTTCNDFASSGDPNYNLIYSMCLTLLGFLIPLFVM	180
Qy	200	CFFYYKMVFLKRRSQQQATALPLDKPQRLVVLAVVIFSILEFTPYHIMRNLRIASRLDSW	259
		: : : : : : : : : :	
Db	181	CFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVLFTPYHVMRNVRIASRLGSW	240
Qy	260	PQ-GCTQKAIKSIYTLTR	276
		:	
Db	241	KQYQCTQVVINSFYIVTR	258

Search completed: August 23, 2004, 17:00:22
 Job time : 132 secs

OM protein - protein search, using sw model

Run on: August 23, 2004, 16:58:14 ; Search time 31 Seconds
 (without alignments)
 527.917 Million cell updates/sec

Title: US-09-891-138A-2
 Perfect score: 1650
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Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents AA:*
 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		Match Length DB			ID	Description
	Score	Match	Length	DB	ID		
1	1226.5	74.3	334	2	US-08-559-524A-2		Sequence 2, Appli
2	1226.5	74.3	334	3	US-08-749-707-2		Sequence 2, Appli
3	1226.5	74.3	334	4	US-09-947-922-2		Sequence 2, Appli
4	474	28.7	373	2	US-08-559-524A-4		Sequence 4, Appli
5	474	28.7	373	3	US-08-749-707-4		Sequence 4, Appli
6	474	28.7	373	4	US-09-947-922-4		Sequence 4, Appli
7	473.5	28.7	362	3	US-08-513-974B-374		Sequence 374, App
8	372	22.5	374	4	US-09-102-710B-3		Sequence 3, Appli
9	370.5	22.5	373	3	US-08-513-974B-373		Sequence 373, App
10	353	21.4	355	1	US-08-153-848-28		Sequence 28, Appl
11	353	21.4	355	1	US-08-153-848-32		Sequence 32, Appl

12	353	21.4	355	3	US-09-299-843A-28	Sequence 28, Appl
13	353	21.4	355	3	US-09-299-843A-32	Sequence 32, Appl
14	353	21.4	355	4	US-09-088-337B-28	Sequence 28, Appl
15	353	21.4	355	4	US-09-088-337B-32	Sequence 32, Appl
16	353	21.4	355	4	US-09-170-496D-130	Sequence 130, App
17	353	21.4	355	4	US-09-170-496D-232	Sequence 232, App
18	353	21.4	355	5	PCT-US93-11153-28	Sequence 28, Appl
19	353	21.4	355	5	PCT-US93-11153-32	Sequence 32, Appl
20	338	20.5	328	3	US-08-513-974B-39	Sequence 39, Appl
21	338	20.5	328	3	US-08-513-974B-371	Sequence 371, App
22	338	20.5	328	4	US-09-461-436B-39	Sequence 39, Appl
23	336.5	20.4	360	3	US-08-875-573-20	Sequence 20, Appl
24	336.5	20.4	360	3	US-09-232-878-2	Sequence 2, Appli
25	336.5	20.4	360	3	US-09-045-583-55	Sequence 55, Appl
26	336.5	20.4	360	4	US-09-534-185-55	Sequence 55, Appl
27	336.5	20.4	360	4	US-08-939-107-34	Sequence 34, Appl
28	335.5	20.3	375	1	US-08-442-134A-2	Sequence 2, Appli
29	335.5	20.3	375	1	US-08-444-581B-2	Sequence 2, Appli
30	335.5	20.3	375	1	US-08-446-088A-2	Sequence 2, Appli
31	335.5	20.3	375	2	US-08-559-524A-3	Sequence 3, Appli
32	335.5	20.3	375	3	US-08-749-707-3	Sequence 3, Appli
33	335.5	20.3	375	4	US-09-947-922-3	Sequence 3, Appli
34	329	19.9	355	3	US-09-045-583-53	Sequence 53, Appl
35	329	19.9	355	4	US-09-534-185-53	Sequence 53, Appl
36	328	19.9	355	1	US-08-012-988A-2	Sequence 2, Appli
37	328	19.9	355	1	US-08-450-393A-5	Sequence 5, Appli
38	328	19.9	355	3	US-08-446-669-5	Sequence 5, Appli
39	328	19.9	355	4	US-09-239-938-1	Sequence 1, Appli
40	328	19.9	355	4	US-09-886-319A-14	Sequence 14, Appl
41	328	19.9	355	5	PCT-US95-00476-5	Sequence 5, Appli
42	326.5	19.8	360	4	US-08-833-752-10	Sequence 10, Appl
43	325.5	19.7	346	4	US-09-585-876-2	Sequence 2, Appli
44	325	19.7	302	2	US-08-467-948A-30	Sequence 30, Appl
45	325	19.7	302	3	US-08-467-947A-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1

US-08-559-524A-2

; Sequence 2, Application US/08559524A

; Patent No. 5871963

; GENERAL INFORMATION:

; APPLICANT: Conley, Pamela B.

; APPLICANT: Jantzen, Hans-Michael

; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP

; STREET: 1800 M Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20036-5869

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

```

;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/559,524A
;      FILING DATE:  15-NOV-1995
;      CLASSIFICATION:  435
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Adler, Reid G.
;      REGISTRATION NUMBER:  30,988
;      REFERENCE/DOCKET NUMBER:  044481-5010-00-US
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-467-7000
;      TELEFAX:  202-467-7176
;      INFORMATION FOR SEQ ID NO:  2:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  334 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  protein
US-08-559-524A-2

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Query Match          74.3%;  Score 1226.5;  DB 2;  Length 334;
Best Local Similarity  71.5%;  Pred. No. 4.7e-93;
Matches 226;  Conservative  42;  Mismatches  47;  Indels    1;  Gaps    1;

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Qy      1 MAQNLSCEWNLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLCMKWNSSNVYLEN 60
      || | :|:|||| || | ||||| || |||: |:|| | |:|:| :|:||||:|:|
Db      5 MAWNATCKNWLAAEAALKEYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLEN 64

Qy     61 LSISDFAFLCTLPLILIKSYANDKGTYGDLVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
      ||:| | |||||:|:| || | ||||| ||||| |||||:|:|:|
Db     65 LSVSDLAFCLTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

Qy    121 KYPFREHFLQKKEFAILISLAWWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHN 180
      ||||| | ||||| |||||:| |||||:|:| || | : | : | |:|:|:| :|
Db    125 KYPFREHLLQKKEFAILISLAIWVLTLELLPLPLINPVITDNGTTCNDFASSGDPNYN 184

Qy    181 LIYSLCLTLLGFLIPLSVMCFFYYKMVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
      ||||:| ||||| ||||| |||||:| :|:|:|:| |||||:| | |:| |||||:|
Db    185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL 244

Qy    241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
      ||||:|:|:| |||| || | || | || | :|| | |||| |:|:|:|:|:|:|
Db    245 FTPYHVMRNVRIASRLGSKQYQCTQVVINSFYIVTRALGFLNSVINPVFYFLLGDHFRD 304

Qy    300 MLISKFRQYFKSLTSF 315
      ||::: | |||||
Db    305 MLMNQLRHNFKSLTSF 320

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RESULT 2

US-08-749-707-2

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; Sequence 2, Application US/08749707
; Patent No. 6063582
; GENERAL INFORMATION:
; APPLICANT:  Conley, Pamela B.

```

```

; APPLICANT: Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,707
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044481-5010-01-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-749-707-2

```

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Query Match          74.3%; Score 1226.5; DB 3; Length 334;
Best Local Similarity 71.5%; Pred. No. 4.7e-93;
Matches 226; Conservative 42; Mismatches 47; Indels 1; Gaps 1;

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QY      1 MAQNLSCEWNLATEAILNKYYLSAFYAIEFIFGLLGNTVTVVFGYLFCKMKNWNSSNVYLEN 60
      || | :|:|||| || | |||| || |||: |:|| | |:|:| :|:|:|:|:|
Db      5 MAWNATCKNWLAAEALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLEN 64

QY      61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDDRYLLM 120
      ||:| | |||||:|:| || | ||||| ||||| |||||:|:|:|:|:|
Db      65 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

QY      121 KYPFREHFLQKKEFAILISLAWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHN 180
      ||||| | |||||:|:| ||||:|:| || | : |: | |:|:|:| :|
Db      125 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 184

QY      181 LIYSLCLTLLGFLIPLSVMCFFYYKMVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
      ||||:| ||||| |||||:|:|:|:| |||||:| | |:|:|:|:|
Db      185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSIL 244

QY      241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
      ||||:| |:|:| || | || | || | :| | || | |:|:|:|:|:|
Db      245 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRALGFLNSVINPVFYFLLGDHFRD 304

```

Qy 300 MLISKFRQYFKSLTSF 315
 ||::: | |||||
 Db 305 MLMNQLRHNFKSLTSF 320

RESULT 3

US-09-947-922-2

; Sequence 2, Application US/09947922
 ; Patent No. 6680373
 ; GENERAL INFORMATION:
 ; APPLICANT: Conley, Pamela B.
 ; Jantzen, Hans-Michael
 ; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
 ; STREET: 1800 M Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20036-5869
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/947,922
 ; FILING DATE: 07-Sep-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/749,707
 ; FILING DATE: 15-NOV-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Adler, Reid G.
 ; REGISTRATION NUMBER: 30,988
 ; REFERENCE/DOCKET NUMBER: 044481-5010-01-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-467-7000
 ; TELEFAX: 202-467-7176
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 334 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-947-922-2

Query Match 74.3%; Score 1226.5; DB 4; Length 334;
 Best Local Similarity 71.5%; Pred. No. 4.7e-93;
 Matches 226; Conservative 42; Mismatches 47; Indels 1; Gaps 1;

Qy 1 MAQNLSCEWNLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCKMKNWNSSNVYLFN 60
 || | :||| || | |||| || ||| :|:| | |:|:| :|||:|
 Db 5 MAWNATCKNWLAEEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 64

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; Sequence 4, Application US/08559524A
; Patent No. 5871963
; GENERAL INFORMATION:
;   APPLICANT: Conley, Pamela B.
;   APPLICANT: Jantzen, Hans-Michael
;   TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
;     STREET: 1800 M Street, N.W.
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: USA
;     ZIP: 20036-5869
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/559,524A
;   FILING DATE: 15-NOV-1995
;   CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;   NAME: Adler, Reid G.
;   REGISTRATION NUMBER: 30,988
;   REFERENCE/DOCKET NUMBER: 044481-5010-00-US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202-467-7000
;   TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 373 amino acids

```

```
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  protein
US-08-559-524A-4
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Query Match          28.7%;  Score 474;  DB 2;  Length 373;
Best Local Similarity 36.6%;  Pred. No. 2.3e-31;
Matches 105;  Conservative 58;  Mismatches 116;  Indels 8;  Gaps 6;
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```
Qy      20 YYLSAFYAIEFIFGLLGNTVVFGYLFCKMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79
      ||| | | : || | ||| :: ::| || | : ||:||||::|| :: ||| || |
Db      52 YYLPAVYILVFIIGFLGNSVAIWFMFVFMKPSGISVYMFNLALADFLYVLTLPALIFY 111

Qy      80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTIFISMDRYLLMKYPFREHFLQKKEFAILI 138
      |      :|| :| |:: | ||| ||||| || || : || : ||: ||: |
Db      112 FNKTDWIFGDAMCKLQRFIFHVNLGYSILFLTICISAHRYSGVVYPLKSLGRLKKKNVYI 171

Qy      139 SLAVWALVTLEVLPLMTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
      |: || :| : : |:| : : : | : | | | |||:| |: | :||
Db      172 SVLVWLIVVVGISPILFYSGTGIRKNKTITCYDTSDEYLRSYFIYSMCTTVAMFCVPLV 231

Qy      198 VMCFFYYKMVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILETPYHIMRNLRIASRL 256
      :: | :| | : : || | ||:: : :|:: : |:|:|: : : :||
Db      232 LILGCYGLIVRALIYKDLDNS---PLRRKSIYLVIIIVLTVFAVSYPHFVMTMNLRLARL 288

Qy      257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
      | | : | : : | :|| || ||| ::|| ||| || :| |
Db      289 DFQTPMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335
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RESULT 5

US-08-749-707-4

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; Sequence 4, Application US/08749707
; Patent No. 6063582
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,707
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
```

```

; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044481-5010-01-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 373 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-749-707-4

```

```

Query Match          28.7%; Score 474; DB 3; Length 373;
Best Local Similarity 36.6%; Pred. No. 2.3e-31;
Matches 105; Conservative 58; Mismatches 116; Indels 8; Gaps 6;

```

```

Qy      20 YYLSAFYAIEFIFGLLGNTVVFGYLFCKMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79
      ||| | | : || | ||| :: ::| || | : ||:||||::|| :: ||| || |
Db      52 YYLPAVYILVFIIGFLGNSVAIWMFVFMKPWSGISVYMFNLALADFLYVLTLPALIFY 111

Qy      80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFSMDRYLLMKYPFREHFLQKKEFAILI 138
      | :|| :| |:: | ||| ||||| || || : || : ||: ||: |
Db      112 FNKTDWIFGDAMCKLQRFIFHVNLGYLSILFLTCSAHRYSGVVYPLKSLGRLKKKNVYI 171

Qy      139 SLAVWALVTLEVLPLMTFINS--VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
      |: || :| : : |:| : : : | : | | | |||:| |: | :||
Db      172 SVLVWLIVVVGISPILFYSGTGIRKNKTITCYDTSDEYLRSYFIYSMCTTVAMFCVPLV 231

Qy      198 VMCFFYYKMVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILETPYHIMRNLRIASRL 256
      :: | :| | : : || | ||:: : :||: : |:|:|: : : :||
Db      232 LILGCYGLIVRALIYKDLDNS---PLRRKSIYLVIIVLTVFAVSYPFHVMKTMNLRARL 288

Qy      257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
      | |: | : : | :|| || ||| ::|| ||| || :| |
Db      289 DFQTPMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335

```

RESULT 6

US-09-947-922-4

; Sequence 4, Application US/09947922

; Patent No. 6680373

; GENERAL INFORMATION:

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; APPLICANT: Conley, Pamela B.
; Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:

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```

;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/947,922
;           FILING DATE: 07-Sep-2001
;           CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US/08/749,707
;           FILING DATE: 15-NOV-1996
;
; ATTORNEY/AGENT INFORMATION:
;           NAME: Adler, Reid G.
;           REGISTRATION NUMBER: 30,988
;           REFERENCE/DOCKET NUMBER: 044481-5010-01-US
;
; TELECOMMUNICATION INFORMATION:
;           TELEPHONE: 202-467-7000
;           TELEFAX: 202-467-7176
;
; INFORMATION FOR SEQ ID NO: 4:
;           SEQUENCE CHARACTERISTICS:
;           LENGTH: 373 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: <Unknown>
;           TOPOLOGY: linear
;
;           MOLECULE TYPE: protein
;           SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-947-922-4

```

```

Query Match          28.7%; Score 474; DB 4; Length 373;
Best Local Similarity 36.6%; Pred. No. 2.3e-31;
Matches 105; Conservative 58; Mismatches 116; Indels 8; Gaps 6;

```

```

Qy      20 YYLSAFYAIEFIFGLLGNVTVVFGYLFCKMKNWNSSNVYLEFNLSISDFAFLCTLPILIKSY 79
      ||| | | : || | ||| : : || | | : ||: ||| : : || : || | |
Db      52 YYLPAVYIILVFIIGFLGNSVAIWMFVHMKPWSGISVYMFNLALADFLYVLTLPALIFY 111

Qy      80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILI 138
      | : || : | | : | || | || || | | | : || : || : | : |
Db      112 FNKTDWIFGDAMCKLQRFIFHVNLGYLSILFLTCISAHRYSGVVYPLKSLGRLLKKKNVYI 171

Qy      139 SLAVWALVTLEVLPLMTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
      | : || : | : : | : | : : | : | | | | | || : | : | : ||
Db      172 SVLVWLI VVGISPILFYSGTGIRKNKTITCYDTSDEYLRSYFIYSMCTTVAMFCVPLV 231

Qy      198 VMCFYYKMMVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIRASRL 256
      : : | : | | : : | | | | | : : : : | : | : : : : ||
Db      232 LILGCYGLIVRALIYKDLDNS---PLRRKSIYLVIIIVLTVFAVSYPFHVMKTMNLRARL 288

Qy      257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
      | | : | : : | : || || ||| : || || || | : | |
Db      289 DFQTPMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335

```

```

RESULT 7
US-08-513-974B-374
; Sequence 374, Application US/08513974B
; Patent No. 6114139

```

; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1945
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 374:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 362 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-513-974B-374

```

```

Query Match          28.7%; Score 473.5; DB 3; Length 362;
Best Local Similarity 35.9%; Pred. No. 2.4e-31;
Matches 110; Conservative 57; Mismatches 122; Indels 17; Gaps 8;

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```

Qy      10 WLA----TEAILNK-----YYLSAFYAIEFIFGLLGNTVVFGYLFCKMKNWNSSNVYLEN 60
      | |   | : | |   |||   | : || | |||   :: ::| | : | : ||: ||
Db      22 WAAGNATTKCSLTKTGQFYYPPTVYILVFITGFLGNSVAIWMFVFHMRPWSGISVYMEN 81

Qy      61 LSISDEAFCLCTLPILIKSYANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLL 119
      | ::::| | : ||| || | |   : ||: |   | : | ||| ||||| ||: ||
Db      82 LALADFLYVLTLPALIFYFNKTDWIFGDMCKLQRFIFHVNLVYGSILFLTCISVHRYTG 141

Qy     120 MKYPFREHFLQKKEFAILISLAVWALVTLEVLPLMLTFIN-SVPKEEGSNCIDYASSGNPE 178
      : : | :   ||: | : :| ||||   : | : | :   | : :   | | :
Db     142 VVHPLKSLGRLKKKNAVYVSSLVWALVVAVIAPILFYSGIGVRRNKTITCYDTTADEYLR 201

Qy     179 HNLISYSLCLTLLGFLIPLSVMCFYYKMWVFLKRRSQQQATALPL-DKPQRLVVLAVVIF 237
      : ||: | | : | || | : | | :   :   || | | ||: : : |
Db     202 SYFVYSMCTTVFMFCIPFIVILGCYGLIVKALIKYKDLDNS---PLRRKSTYLVIIIVLTVF 258

Qy     238 SILFTPYHIMRNLRIASRLD-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGD 295
      :: : | : | : | : : |||   || |   : : | : || || ||| : || ||| ||
Db     259 AVSYLPFHVMKTLNLRARLDFQTPQMCAFNDKVYATYQVTRGLASLNSCVDPILYFLAGD 318

Qy     296 HYREML 301
      : | |
Db     319 TFRRRL 324

```

RESULT 8

US-09-102-710B-3

```

; Sequence 3, Application US/09102710B
; Patent No. 6479630
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Au-Young, Janice
; APPLICANT: Stuart, Susan G.
; TITLE OF INVENTION: A NOVEL HUMAN PURINERGIC P2U RECEPTOR
; FILE REFERENCE: PF-0038-1 DIV

```

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; CURRENT APPLICATION NUMBER: US/09/102,710B
; CURRENT FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: RNU09402
US-09-102-710B-3
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```
Query Match          22.5%; Score 372; DB 4; Length 374;
Best Local Similarity 33.8%; Pred. No. 5.1e-23;
Matches 96; Conservative 49; Mismatches 125; Indels 14; Gaps 7;
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QY      19 KY-YLSAFYAIEFIFGLLGNTVVFVGYLFCMKNNWSSNVYLFNLSISDFAFLCTLPILIK 77
      || | | : : || || :: : | : | ||: | |:|:|:| | : :||:|:
Db      32 KYVLLPVSYGVVCVLGLCLNVVALYIFLCRLKTWNASTTYMFHLAVSDSLYAASLPLLVY 91

QY      78 SYA-NDKGTYGDLVLCISNRYVLHTNLYTSILFLTTFISMDRYLLMKYPFREHFLQKKEFAI 136
      || | : ||| |:: :||| ||||| ||: | | : | :|
Db      92 YYAQGDHWPFTVLCKLVRFLEYTNLYCSILFLTCISVHRSLGVLRLHSLRWGHARYAR 151

QY     137 LISLAVWALVTLEVLPMPLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPL 196
      :: || || | : | : : : | | : | : || : | | : |
Db     152 RVAAVVWVLVLACQTPVLYFVTTSVRGTRITCHDTSRELFSSHVAYSSVMLGLLFAVPF 211

QY     197 SVMCFYYKMWVFLKRRSQQA---TALPLDKPQ--RLVVLAUVIFSILETPYHIMRNLR 251
      |:: | | : || : | | || | : | : | : :|:| | | |
Db     212 SIILVCY----VLMARRLLKPAYGTGLPRAKRKSVRTIALVLAVFALCFLPFHVTRTLY 267

QY     252 IASRLDSWPQGC-TQKAIKSIYTLTRPLAFLNSAINPIFYFLMG 294
      : | | | | || | : |||| | || :|:| | || |
Db     268 YSFR--SLDLSCHTLNAINMAYKITRPLASANSCLDPVLYFLAG 309
```

RESULT 9

US-08-513-974B-373

; Sequence 373, Application US/08513974B

; Patent No. 6114139

; GENERAL INFORMATION:

; APPLICANT: Hinuma, Shuji

; APPLICANT: Hosoya, Masaki

; APPLICANT: Fujii, Ryo

; APPLICANT: Ohtaki, Tetsuya

; APPLICANT: Fukusumi, Shoji

; APPLICANT: Ohgi, Kazuhiro

; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,

; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF

; NUMBER OF SEQUENCES: 380

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

; STREET: 130 Water Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1945
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 373:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 373 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
US-08-513-974B-373

Query Match 22.5%; Score 370.5; DB 3; Length 373;
Best Local Similarity 33.5%; Pred. No. 6.8e-23;
Matches 94; Conservative 50; Mismatches 130; Indels 7; Gaps 5;

Qy 19 KY-YLSAFYAIEFIFGLLGNTVVFGYLFCKMKNWNSSNVYLFNLSISDFAFLCTLPILIK 77
|| | : : || || :: : | : || : | : | : | : | : : || : :
Db 32 KYVLLPVSYGVVCLVGLCLNVVALYIFLCRLKIWNASTTYMFHLAVSDSLYAASLPLLVY 91

Qy 78 SYA-NDKGTYGDLVCISNRYVLHTNLYTSILFLTIFISMDRYLLMKYPFREHFLQKKEFAI 136
|| | : || | : : : || || || || || || : | : | : : |
Db 92 YYARGDHWPFSTVLCKLVRFLEYTNLYCSILFLTICISVHRCGLGVLRLHSLRWGRARYAR 151

Qy 137 LISLAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPL 196
: : || || | : | : : : | | : : | : || : | : | : |
Db 152 RVAAVVWVLVLACQAPVLYFVTTSVRGTRITCHDTSARELFSHFVAYSSVMLGLLFAVPF 211

Qy 197 SVMCFFYYKMVFLKRRSQQQATALPLDKPQ--RLVVLAVVIFSILFTPYHIMRNLRIAS 254
|| : | | | : : || | : | : | : : : | : | : | : | :
Db 212 SVILVCYVLMARRLLKPAYGTTGGLPRAKRKSVRTIALVLAVFALCFPLPHVTRTLYYSF 271

Qy 255 RLDSWPQGC-TQKAIKSIYTLTRPLAFLNSAINPIFYFLMG 294
| | | | || | : || || || : : : || |
Db 272 R--SLDLSCHTLNAINMAYKITRPLASANSCLDPVLYFLAG 310

RESULT 10

US-08-153-848-28

; Sequence 28, Application US/08153848

; Patent No. 5759804

; GENERAL INFORMATION:

; APPLICANT: Godiska, Ronald

; APPLICANT: Gray, Patrick W.

; APPLICANT: Schweikart, Vicki L.

; TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

; ADDRESSEE: Bicknell

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/153,848

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/977,452

```

; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-153-848-28

```

```

Query Match          21.4%; Score 353; DB 1; Length 355;
Best Local Similarity 28.1%; Pred. No. 1.7e-21;
Matches 84; Conservative 66; Mismatches 133; Indels 16; Gaps 6;

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Qy      16 ILNKYYLSAFYAIEFIFGLLGNVTVVFGYLEFCMKNWNSSNVYLENLSISDFAFLCTLPIL 75
      :   :|| ||:: | ||:|: |||   | : ::|| ||::|| | : |||
Db      28 VFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKKPKSVTDIYLLNLALSDDLLEFVATLPFW 87

Qy      76 IKSYANDKGTYGDLVCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFA 135
      |::| : : :|   : || |:| ||:|||| :   : :
Db      88 THYLINEKGLH-NAMCKFTTAAFFFIGFFGSIFFITVISIDRYLAIVLAANSNMNRTVQHG 146

Qy     136 ILISLAVWALVTLEVLPLMTFINSVPKEEGSNCI-DYASSGNPEHNLIYSLCLTLLGFLI 194
      : ||| ||| | | | |:: : |: ||   :: :: |||:
Db     147 VTISLGVWAAAILVAAPQFMF-----TKQKENECLGDYPEVLQEIWVPLRVNVTNFLGFL 202

Qy     195 PLSVMCFFYYKMV-VFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLR 253
      || :| : |::: : : :| |:   :|::| |::| : :|||::| |
Db     203 PLLIMSYCYFRIIQTLFSCKNHKKAKAI-----KLILLVVIVFFLEWTPYNVMIFLET 256

Qy     254 SRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQYFKSL 312
      | :|   :| :: :| :|| : :||: | | : :| | : | | |
Db     257 KLYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKFRRYL---YHLYGKCL 312

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RESULT 11

US-08-153-848-32

; Sequence 32, Application US/08153848

; Patent No. 5759804

; GENERAL INFORMATION:

; APPLICANT: Godiska, Ronald

; APPLICANT: Gray, Patrick W.

; APPLICANT: Schweikart, Vicki L.

; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

; ADDRESSEE: Bicknell

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

```

; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-153-848-32

```

```

Query Match          21.4%; Score 353; DB 1; Length 355;
Best Local Similarity 28.1%; Pred. No. 1.7e-21;
Matches 84; Conservative 66; Mismatches 133; Indels 16; Gaps 6;

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Qy      16 ILNKYYLSAFYAIEFIFGLLGNVTVVFGYLEFCMKNWNSSNVYLEFNLSISDFAFLCTLPLIL 75
      :  :|| ||:: | ||::|: |||      | : ::|| ||::|| | : |||
Db      28 VFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKKPKSVTDIYLLNLALSDLLFVATLPFW 87

Qy      76 IKSANDKGTYGDLVCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFA 135
      |:|| : : :|      : || |:| ||:|||| :      : :
Db      88 THYLINEKGLH-NAMCKFTTAFFFIGFFGSIFFITVISIDRYLAIVLAANSMMNRTVQHG 146

Qy     136 ILISLAVWALVTLEVLPLMTFINSVPKEEGSNCI-DYASSGNPEHNLIYSLCLTLLGFLI 194
      : ||| ||| | | | | | : : : | : ||      : : : | |||:
Db     147 VTISLGVWAAAILVAAPQFMF----TKQKENEC LGDYPEVLQEIWPVLRNVETNFLGFL 202

Qy     195 PLSVMCFFYYKMV-VFLKRRSQQQATALPLDKPQRLVVLAVVIFSILETPYHIMRNLRIA 253
      || :| : |::: : : :| | : : :| |::| |::| : :|||::| |
Db     203 PLLIMSYCYFRIIQTLFSCKNHKKAKAI-----KLILLVVIVFFLFWTPYNVMIFLET 256

Qy     254 SRLDSWPQGCTQKAIKSIYTLTRPLAFINSAINPIFYFLMGDHYREMLISKFRQYFKSL 312
      | :| :| : : :| :|| : :||: | | : :| | : | | |
Db     257 KLYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKFRRYL---YHLYGKCL 312

```

RESULT 12

US-09-299-843A-28
; Sequence 28, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-28

Query Match 21.4%; Score 353; DB 3; Length 355;
Best Local Similarity 28.1%; Pred. No. 1.7e-21;
Matches 84; Conservative 66; Mismatches 133; Indels 16; Gaps 6;

Qy 16 ILNKYYLSAFYAIEFIFGLLGNVTVVFGYLEFCMKNWNSSNVYLEFNLSISDF AFLCTLPIL 75
: :|| ||:: | ||:||: ||| | : ::|| ||::|| |: |||

Db 28 VFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKKPKSVTDIYLLNLALSDLLFVATLPFW 87

Qy 76 IKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFA 135
 :|| : : :| : || :| ||:|||| : : :

Db 88 THYLINEKGLH-NAMCKFTTAFFFIGFFGSIFFITVISIDRYLAIVLAANSMMNRVTQHG 146

Qy 136 ILISLAVWALVTLEVLPMPLTFINSVPKEEGSNCI-DYASSGNPEHNLIYSLCLTLLGFLI 194
 : ||| ||| | | | | :| : : || : : : |||:

Db 147 VTISLGWAAAILVAAPQFMF-----TKQKENECLGDYPEVLQEIWVLRNVETNFGFL 202

Qy 195 PLSVMCFFYYKMV-VFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIA 253
 || :| : |::: : : :| | : :| | :| :| :| :| :| :

Db 203 PLLIMSYCYFRIIQTLSCKNHKKAKAI-----KLILLVIVFFLFWTPYNVMIFLET 256

Qy 254 SRLDSWPQGCTQKAISYITLRLPLAFLNSAINPIFYFLMGDHYREMLISKFRQYFKSL 312
 | :| :| : : :| :| : :| :| :| :| :| :| :| :

Db 257 KLYDFFPSCDMRDLRLALSVTETVAFSHCCLNPLIYAFAGEKFRRYL---YHLYGKCL 312

RESULT 13

US-09-299-843A-32

; Sequence 32, Application US/09299843A

; Patent No. 6107475

; GENERAL INFORMATION:

; APPLICANT: Godiska, Ronald

; APPLICANT: Gray, Patrick W.

; APPLICANT: Schweikart, Vicki L.

; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

; ADDRESSEE: Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/299,843A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 09/088,337

; FILING DATE: 01-JUN-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/153,848

; FILING DATE: 17-NOV-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/977,452

; FILING DATE: 17-NOV-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Jill E. Uhl

```

;     REGISTRATION NUMBER: 43,213
;     REFERENCE/DOCKET NUMBER: 27866/32059B
;     TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (312) 474-6300
;     TELEFAX: (312) 474-0448
;     TELEX:
;     INFORMATION FOR SEQ ID NO: 32:
;     SEQUENCE CHARACTERISTICS:
;     LENGTH: 355 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-09-299-843A-32

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Query Match          21.4%; Score 353; DB 3; Length 355;
Best Local Similarity 28.1%; Pred. No. 1.7e-21;
Matches 84; Conservative 66; Mismatches 133; Indels 16; Gaps 6;

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Qy      16 ILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCKMKNWNSSNVYLFNLSISDFAFLCTLPIL 75
      :   :|| ||:: | ||:|: || | : ::|| ||::|| | : |||
Db      28 VFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKKPKSVTDIYLLNLALSDLLFVATLPFW 87

Qy      76 IKSANDKGTYGDLVCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFA 135
      |:|| : : :| : || ||: ||| : : :
Db      88 THYLINEKGLH-NAMCKFTTAAFFFIGFFGSIFFITVISIDRYLAIVLAANSMMNRTVQHG 146

Qy     136 ILISLAWWALVTLEVLPLMTFFINSVPKEEGSNCI-DYASSGNPEHNLIYSLCLTLLGFLI 194
      : ||| ||| | | | | : : : | : || : : : |||:
Db     147 VTISLGVWAAAILVAAPQFMF-----TKQKENECLGDYPEVLQEIWPVLRNVETNFLGFL 202

Qy     195 PLSVMCFFYYKMV-VFLKRRSQQQATALPLDKPQRLVVLAVVIFSILETPYHIMRNLRIA 253
      || :| : |::: : : :| | : : :| |::| : :|||::| |
Db     203 PLLIMSYCYFRIIQTLFSCKNHKKAKAI-----KLILLVVIVFFLEFWTPYNVMIFLET 256

Qy     254 SRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQYFKSL 312
      | :| :| : : :| :|| : :||: | | : :| | : |||
Db     257 KLYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKFRRYL---YHLYGKCL 312

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RESULT 14

US-09-088-337B-28

; Sequence 28, Application US/09088337B

; Patent No. 6348574

; GENERAL INFORMATION:

; APPLICANT: Godiska, Ronald

; Gray, Patrick W.

; Schweikart, Vicki L.

; TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

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;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.25
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/088,337B
;      FILING DATE: 01-Jun-1998
;      CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US 08/153,848
;      FILING DATE: 17-NOV-1993
;      APPLICATION NUMBER: US 07/977,452
;      FILING DATE: 17-NOV-1992
;      ATTORNEY/AGENT INFORMATION:
;      NAME: No. 6348574and, Greta E.
;      REGISTRATION NUMBER: 35,302
;      REFERENCE/DOCKET NUMBER: 31794
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (312) 474-6300
;      TELEFAX: (312) 474-0448
;      TELEX: 25-3856
;      INFORMATION FOR SEQ ID NO: 28:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 355 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-088-337B-28

```

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Query Match          21.4%;  Score 353;  DB 4;  Length 355;
Best Local Similarity 28.1%;  Pred. No. 1.7e-21;
Matches 84;  Conservative 66;  Mismatches 133;  Indels 16;  Gaps 6;

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```

Qy      16 ILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLEFNLSISDEAFCLTLPIL 75
      :      :|| ||:: | ||::| | |      | : ::|| ||::|| | : |||
Db      28 VFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKKPKSVTDIYLLNLALSDDLLEVATLPFW 87

Qy      76 IKSANDKGTGVDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFA 135
      |:|| : : :|      : || |:| ||:|||| :      : :
Db      88 THYLINEKGLH-NAMCKFTTAAFFFIGFFGSIFFITVISIDRYLAIVLAANSMMNRTVQHG 146

Qy      136 ILISLAVWALVTLEVLPLMTFINSVPKEEGSNCI-DYASSGNPEHNLIYSLCLTLLGFLI 194
      : ||| ||| | | | | | : : : | : ||      : : : | ||| :
Db      147 VTISLGVWAAAILVAAPQFMF----TKQKENECLGDYPEVLQEIWPVLRNVETNFGFL 202

Qy      195 PLSVMCFFYYKMV-VFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIA 253
      || :| : |::: : : :| | : : :| | : :| | : :| | : :| | : |
Db      203 PLLIMSYCYFRIIQTLSCKNHKKAKAI-----KLILLVVIVFFLFWTPYNVMIFLET 256

Qy      254 SRLDSWPQGCTQKAKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQYFKSL 312
      | :| :| : : :| :|| : :||: | | : :| | : :| |
Db      257 KLYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKFRRYL---YHLYGKCL 312

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RESULT 15

US-09-088-337B-32
; Sequence 32, Application US/09088337B
; Patent No. 6348574
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; Gray, Patrick W.
; Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,337B
; FILING DATE: 01-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6348574and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-088-337B-32

Query Match 21.4%; Score 353; DB 4; Length 355;
Best Local Similarity 28.1%; Pred. No. 1.7e-21;
Matches 84; Conservative 66; Mismatches 133; Indels 16; Gaps 6;

Qy 16 ILNKYYLSAFYAIEFIFGLLGNVTVVFGYLCMKNNSSNVYLFNLSISDFAFLCTLPIIL 75
: :|||::| ||::| | : ::|||::| | : |||
Db 28 VFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKKPKSVTDIYLLNLALSDDLFFVATLPFW 87
Qy 76 IKSANDKGTGYDVLCSNRYVLHTNLYTSILFLTFSMDRYLLMKYPFREFHFLQKKEFA 135

Db	88	THYLINEKGLH-NAMCKFTTAAFFFIGFFGSIFFITVISIDRYLAIVLAANSMNNRTVQHG	146
Qy	136	ILISLAVWALVTLEVLPLMTFINSVPKEEGSNCI-DYASSGNPEHNLIYSLCLTLLGFLI	194
Db	147	VTISLGVWAAAILVAAPQFMF----TKQKENECLGDYPEVLQEIWPVLRNVETNFLGFL	202
Qy	195	PLSVMCFFYYKMV-VFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIA	253
Db	203	PLLIMSYCYFRIIQTLEFSCKNHKKAKAI-----KLILLVVIVFFLFWTPYNVMIFLETL	256
Qy	254	SRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQYFKSL	312
Db	257	KLYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKERRYL---YHLYGKCL	312

Search completed: August 23, 2004, 17:04:14
Job time : 33 secs

OM protein - protein search, using sw model

Run on: August 23, 2004, 16:56:04 ; Search time 40 Seconds
(without alignments)
762.318 Million cell updates/sec

Title: US-09-891-138A-2
Perfect score: 1650
Sequence: 1 MAQNLSCEWNLATEAILNKY.....REMLISKFRQYFKSLTSFRT 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	474	28.7	373	2	JC4162	P2Y receptor - bov
2	474	28.7	373	2	JC4737	G protein-coupled
3	472.5	28.6	362	2	S33733	G protein-coupled
4	373.5	22.6	373	2	A47556	ATP receptor P2u -
5	353	21.4	355	2	JC4304	orphan G protein-c
6	352	21.3	365	2	S68679	G protein-coupled
7	336.5	20.4	360	2	A57160	chemokine (C-C) re
8	336	20.4	328	2	I55450	G protein-coupled
9	335.5	20.3	375	2	A54946	P-2U nucleotide re
10	333	20.2	308	2	I50241	G protein-coupled
11	332.5	20.2	354	2	I58186	probable G protein
12	332	20.1	328	2	JC4800	P2Y6 receptor - hu
13	328	19.9	355	2	A45177	chemokine (C-C) re

14	326.5	19.8	360	2	JC4587	chemokine (C-C) re
15	325.5	19.7	388	2	JN0605	somatostatin recep
16	318.5	19.3	359	2	A48921	interleukin-8 rece
17	317.5	19.2	355	2	A55733	G protein-coupled
18	316.5	19.2	384	2	A47249	brain-specific som
19	315.5	19.1	355	2	JQ1231	interleukin-8 rece
20	315	19.1	355	2	JC5067	G protein-coupled
21	314	19.0	369	2	JC2083	somatostatin recep
22	314	19.0	369	2	B41795	somatostatin recep
23	314	19.0	370	2	JC5549	heptahelical P2Y5-
24	313	19.0	344	2	T09508	intron 17 purinerg
25	312.5	18.9	360	2	A53611	interleukin-8 rece
26	311	18.8	358	2	A53752	interleukin-8 rece
27	309.5	18.8	384	2	JC4629	somatostatin recep
28	309	18.7	355	2	I49339	macrophage inflamm
29	308	18.7	369	2	D41795	somatostatin recep
30	307.5	18.6	369	2	A45291	somatostatin recep
31	306	18.5	356	2	I49340	MIP-1 alpha recept
32	306	18.5	362	2	A39714	G protein-coupled
33	306	18.5	391	2	A39297	somatostatin recep
34	305	18.5	346	2	S29248	somatostatin recep
35	304.5	18.5	361	2	B45680	G protein-coupled
36	303	18.4	350	2	A39445	interleukin-8 rece
37	303	18.4	391	2	A41795	somatostatin recep
38	303	18.4	391	2	C41795	somatostatin recep
39	302	18.3	366	1	OORTB2	bradykinin recepto
40	301.5	18.3	369	2	JC5068	G protein-coupled
41	301	18.2	355	2	G02436	chemokine (C-C) re
42	299.5	18.2	353	2	A53858	bradykinin recepto
43	298	18.1	354	2	T09353	G protein-coupled
44	297	18.0	387	2	I69202	G protein-coupled
45	295.5	17.9	363	2	I57955	somatostatin recep

ALIGNMENTS

RESULT 1

JC4162

P2Y receptor - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 12-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 24-Sep-1999

C;Accession: JC4162

R;Henderson, D.J.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.

Biochem. Biophys. Res. Commun. 212, 648-656, 1995

A;Title: Cloning and characterisation of a bovine P2Y receptor.

A;Reference number: JC4162; MUID:95352058; PMID:7626079

A;Accession: JC4162

A;Molecule type: mRNA

A;Residues: 1-373 <HEN>

A;Cross-references: EMBL:X87628; NID:g1032484; PIDN:CAA60958.1; PID:g1032485

A;Experimental source: aortic endothelial cell

C;Genetics:

A;Gene: bovp2y

C;Superfamily: ATP receptor P2u

C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein

F;52-77/Domain: transmembrane #status predicted <TM1>

F;88-111/Domain: transmembrane #status predicted <TM2>
 F;124-150/Domain: transmembrane #status predicted <TM3>
 F;171-191/Domain: transmembrane #status predicted <TM4>
 F;214-237/Domain: transmembrane #status predicted <TM5>
 F;261-282/Domain: transmembrane #status predicted <TM6>
 F;305-328/Domain: transmembrane #status predicted <TM7>
 F;11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;258/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 28.7%; Score 474; DB 2; Length 373;
 Best Local Similarity 36.6%; Pred. No. 4e-32;
 Matches 105; Conservative 58; Mismatches 116; Indels 8; Gaps 6;

```

Qy      20 YYLSAFYAIEFIFGLLGNVTVVFGYLFCKMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79
      ||| | | : || | ||| :: :| || | : ||:| ||::|| :: ||| || |
Db      52 YYLPAVYILVFIIGFLGNSVAIWMFVHMKPWSGISVYMFNLALADFLYVLTLPALIFY 111

Qy      80 ANDKG-TYGDVLCISNRYVLHTNLTYLSILFLTFSMDRYLLMKYPFREHFLQKKEFAILI 138
      |      :|| :|  :: | ||| ||||| || || : || :      ||: |: |
Db     112 FNKTDWIFGDAMCKLQRFIFHVNLGYSILFLTCSIAHRYSGVVYPLKSLGRLLKKNAVYI 171

Qy     139 SLAVWALVTLEVLPLMTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
      |: || :| : : |:| : : : | : | | | |||:| |: | :||
Db     172 SVLVWLI VVGISPILFYSGTGIRKNKTITCYDTSDEYLRSYFIYSMCTTVAMFCVPLV 231

Qy     198 VMCFFYYKMVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL 256
      :: | :| | : : || | ||:: : :|:: : |:|:|: : : :||
Db     232 LILGCYGLIVRALIYKDLNDS---PLRRKSIYLVIIVLTVFVAVSYIPFHVMTMNLRL 288

Qy     257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
      | | : | : : | :|| || ||| ::|| ||| || :| |
Db     289 DFQTPMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335
  
```

RESULT 2

JC4737

G protein-coupled receptor P2Y1 - human

N;Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor

C;Species: Homo sapiens (man)

C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 17-Nov-2000

C;Accession: JC4737; JC4615; S54253

R;Janssens, R.; Communi, D.; Pirotton, S.; Samson, M.; Parmentier, M.;

Boeynaems, J.M.

Biochem. Biophys. Res. Commun. 221, 588-593, 1996

A;Title: Cloning and tissue distribution of the human P2Y1 receptor.

A;Reference number: JC4737; MUID:96205320; PMID:8630005

A;Accession: JC4737

A;Molecule type: DNA

A;Residues: 1-373 <JAN>

A;Cross-references: GB:S81950; NID:g1839438; PIDN:AAB47091.1; PID:g1839439

R;Ayyanathan, K.; Webbs, T.E.; Sandhu, A.K.; Athwal, R.S.; Barnard, E.A.;
 Kunapuli, S.P.

Biochem. Biophys. Res. Commun. 218, 783-788, 1996

A;Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.

A;Reference number: JC4615; MUID:96158962; PMID:8579591

A;Accession: JC4615

A;Molecule type: mRNA
 A;Residues: 1-373 <AYY>
 A;Cross-references: GB:U42029; NID:g1147730; PIDN:AAA97872.1; PID:g1147731
 A;Experimental source: erythro leukemia cells
 R;Leon, C.; Vial, C.; Cazenave, J.; Gachet, C.
 submitted to the EMBL Data Library, May 1995
 A;Description: Cloning of a human putative P2Y receptor.
 A;Reference number: S54253
 A;Accession: S54253
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-137,139-373 <LEO>
 A;Cross-references: EMBL:Z49205; NID:g798835; PIDN:CAA89066.1; PID:g798836
 C;Comment: This receptor belongs to a family of G protein-coupled receptors. It
 responds to both ADP and ATP, and has several serine/threonine phosphorylation
 residues in the carboxyl terminus.
 C;Genetics:
 A;Gene: p2Y1; GDB:P2RY1
 A;Cross-references: GDB:677125; OMIM:601167
 A;Map position: 3pter-3qter
 C;Superfamily: ATP receptor P2u
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein;
 transmembrane protein
 F;52-77/Domain: transmembrane #status predicted <TM1>
 F;88-111/Domain: transmembrane #status predicted <TM2>
 F;124-152/Domain: transmembrane #status predicted <TM3>
 F;171-191/Domain: transmembrane #status predicted <TM4>
 F;214-237/Domain: transmembrane #status predicted <TM5>
 F;261-282/Domain: transmembrane #status predicted <TM6>
 F;305-328/Domain: transmembrane #status predicted <TM7>
 F;11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;258,336/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status
 predicted
 F;330,339/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status
 predicted
 F;343/Binding site: phosphate (Ser) (covalent) (by protein kinase C and
 calmodulin-dependent kinase) #status predicted

Query Match 28.7%; Score 474; DB 2; Length 373;
 Best Local Similarity 37.3%; Pred. No. 4e-32;
 Matches 107; Conservative 55; Mismatches 117; Indels 8; Gaps 6;

Qy	20	YYLSAFYAIEFIFGLLGNVTVVFGYLCMKNNSSNVYLFNLSISDFAFLCTLPILIKSY	79
		: :: :: : : : :: ::	
Db	52	YYLPAVYILVFIIGFLGNSVAIWMFVFMKPSGIVYMENLALADFLYVLTLPALIFY	111
Qy	80	ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILI	138
		: : :: : : :	
Db	112	FNKTDWIFGDAMCKLQRFIFHVNLGYSLFLTCISAHRYSGVVYPLKSLGRLKKKNAICI	171
Qy	139	SLAVWALVTLEVLPLMTFINS--VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS	197
		: : : : : : : : :	
Db	172	SVLVWLIVVVAISPILFYSGTGVRKNKTITCYDTTSDEYLRSYFIYSMCTTVAMFCVPLV	231
Qy	198	VMCFFYYKMVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILETPYHIMRNLRIRASRL	256
		:: : : : :: : : : : : : : : :	
Db	232	LILGCYGLIVRALIYKDLDNS---PLRRKSIYLVIIIVLTVFAVSYPFHVMKTMNLRARL	288

Qy 257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
 | | | : : | : || || || : || || | : | |
 Db 289 DFQTPAMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335

RESULT 3

S33733

G protein-coupled receptor - chicken

C;Species: Gallus gallus (chicken)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999

C;Accession: S33733

R;Webb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstock, G.; Barnard, E.A.

FEBS Lett. 324, 219-225, 1993

A;Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.

A;Reference number: S33733; MUID:93285340; PMID:8508924

A;Accession: S33733

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-362 <WEB>

A;Cross-references: EMBL:X73268; NID:g395084; PIDN:CAA51716.1; PID:g395085

C;Superfamily: ATP receptor P2u

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 28.6%; Score 472.5; DB 2; Length 362;
 Best Local Similarity 35.9%; Pred. No. 5.2e-32;
 Matches 110; Conservative 58; Mismatches 121; Indels 17; Gaps 8;

Qy 10 WLA----TEAILNK-----YYLSAFYAIEFIFGLLGNTVVFGYLFCKMKNWNSSNVYLEN 60
 | | | : | | | | | : | | | | | : : | | : : | : |
 Db 22 WAAGNATTKCSLTGTGFQFYLLPTVYILVFITGFLGNSVAIWMFVFHMRPWSGISVYMEN 81
 Qy 61 LSISDFAFLCTLPILIKSYANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLL 119
 | : : | : : | | | | | | : | | : | : | | | | | | : | |
 Db 82 LALADFLYVLTLPALIFYFENKTDWIFGDMCKLQRFIFHVNLVYGSILFLTCISVHRYTG 141
 Qy 120 MKYPFREHFLQKKEFAILISLAVWALVTLEVLPLMTFINS-VPKEEGSNCIDYASSGNPE 178
 : : | : | : | : | : | : | : | : | : | : | : | : | :
 Db 142 VVHPLKSLGRLKKKNAVYVSSLVWALVAVIAPILFYSGTGVRNKTITCYDTTADDEYLR 201
 Qy 179 HNLIYSLCLTLLGFLIPLSVMCFYYKMMVFLKRRSQQQATALPL-DKPQRLVVLAVVIF 237
 : | : | : | | | : | : | : | : | : | : | : | : | : | :
 Db 202 SYFVYSMCTTVFMFCIPFIVILGCYGLIVKALIKDLDNS---PLRRKSIYLVIIIVLTVF 258
 Qy 238 SILFTPYHIMRNLRIASRLD-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGD 295
 : : : | : : | : | : | : | : | : | : | : | : | : | : | :
 Db 259 AVSYLPFHVMKTLNLRARLDFQTPQMCAFNKDVYATYQVTRGLASLNSCVDPILYFLAGD 318
 Qy 296 HYREML 301
 : | |
 Db 319 TFRRL 324

RESULT 4

A47556

ATP receptor P2u - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
 C;Accession: A47556
 R;Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.
 Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993
 A;Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.
 A;Reference number: A47556; MUID:93281707; PMID:7685114
 A;Accession: A47556
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-373 <LUS>
 A;Cross-references: GB:L14751; NID:g309457; PIDN:AAA39871.1; PID:g309458
 C;Superfamily: ATP receptor P2u
 C;Keywords: transmembrane protein

Query Match 22.6%; Score 373.5; DB 2; Length 373;
 Best Local Similarity 33.5%; Pred. No. 9.9e-24;
 Matches 94; Conservative 50; Mismatches 130; Indels 7; Gaps 5;

Qy	19	KY-YLSAFYAIEFIFGLLGNVTVVFGYLFCKMKNWNSSNVYLFNLSISDFAFLCTLPLILIK	77
		: : :: : : : : : : : : : :	
Db	32	KYVLLPVSYGVVCVLGLCLNVVALYIFLCRLKTWNASTTYMFHLAVSDSLYAASLPLLVY	91
Qy	78	SYA-NDKGTYGDVLCISNRYVLHTNLYTSILFLTFSMDRYLLMKYPFREHFLQKKEFAI	136
		: :: : : : : :	
Db	92	YYARGDHWPFSTVLCKLVREFLYTNLYCSILFLTCSVHRCGLGVLRLHSLRWGRARYAR	151
Qy	137	LISLAVWALVTLEVLPMLTFINSVPKKEGSNCIDYASSGNPEHNLIYSICLTLLGFLIPL	196
		:: : : : : :: : : :	
Db	152	RVAAVVWVLVLACQAPVLYFVTTSVRGTRITCHDTSARELFSHFVAYSSVMLGLLFAVPF	211
Qy	197	SVMCFYYKMOVFLKRRSQQQATALPLDKPQ--RLVVLAVVIFSILETPYHIMRNLRIAS	254
		: : : : : : : : : :	
Db	212	SVILVCYVLMARRLLKPAYGTTGGLPRAKRKSVRTIALVLAVFALCFLPFHVTRTLYYSF	271
Qy	255	RLDSWPQGC-TQKAIKSIYTLTRPLAFLNSAINPIFYFLMG	294
		: :: :	
Db	272	R--SLDLSCHTLNAINMAYKITRPLASANSCLDPVLYFLAG	310

RESULT 5

JC4304
 orphan G protein-coupled receptor - human
 N;Alternate names: V28 protein
 C;Species: Homo sapiens (man)
 C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
 C;Accession: JC4304
 R;Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
 Gene 163, 295-299, 1995
 A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to genes for chemokine receptors and is expressed in lymphoid and neural tissues.
 A;Reference number: JC4304; MUID:96011651; PMID:7590284
 A;Accession: JC4304
 A;Molecule type: mRNA
 A;Residues: 1-355 <RAP>

A;Cross-references: GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g665581
A;Experimental source: peripheral blood mononuclear cell
C;Comment: This protein is a cell-surface receptor which recognizes extracellular signals and transduces those signals into an intracellular response.
C;Comment: This protein is a key regulator of many immune and homeostatic responses, and interacts between the nervous and immune systems.
C;Genetics:
A;Gene: v28
A;Map position: 3pter-p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
F;35-57/Domain: transmembrane #status predicted <TM1>
F;66-88/Domain: transmembrane #status predicted <TM2>
F;104-125/Domain: transmembrane #status predicted <TM3>
F;146-165/Domain: transmembrane #status predicted <TM4>
F;197-217/Domain: transmembrane #status predicted <TM5>
F;230-254/Domain: transmembrane #status predicted <TM6>
F;275-296/Domain: transmembrane #status predicted <TM7>

Query Match 21.4%; Score 353; DB 2; Length 355;
Best Local Similarity 28.1%; Pred. No. 4.8e-22;
Matches 84; Conservative 66; Mismatches 133; Indels 16; Gaps 6;

```

Qy      16 ILNKYYLSAFYAIEFIFGLLGNVTVVFGYLCMKNNSSNVYLENLSISDFAFLCTLPIIL 75
      :  :|| ||:: | ||:|: |||      | : ::|| ||::|| |: |||
Db      28 VFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKKPKSVTDIYLLNLALSDDLFEVATLPFW 87

Qy      76 IKSYANDKGTYGDLVCISNRYVLHTNLYTSILFLTFSMDRYLLMKYPFREHFLQKKEFA 135
      |:|| : : :|      : || |:| ||:|||| :      : :
Db      88 THYLINEKGLH-NAMCKFTTAAFFFIGFFGSIFFITVISIDRYLAIVLAANSMMNRTVQHG 146

Qy     136 ILISLAVWALVTLEVLPLMTFINSVPKEEGSNCI-DYASSGNPEHNLIYSLCLTLLGFLI 194
      : ||| ||| | | | |:: : |: ||      :: : : ||||:
Db     147 VTISLGWAAAILVAAPQFMF-----TKQKENECLGDYPEVLQEIWVPLRVNVTNFLGFL 202

Qy     195 PLSVMCFFYYKMV-VFLKRRSQQQATALPLDKPQRLVVLAVVIFSILETPYHIMRNLRIA 253
      || :| : |::: : : :|| :      :||:| |:| : :|||::| |
Db     203 PLLIMSYCYFRIIQTLFSCKNHKKAKAI-----KLILLVVIVFFLEWTPYNVMIFLETL 256

Qy     254 SRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQYFKSL 312
      | :| :| :: :|| :|| : :||: | | : :| | : |||
Db     257 KLYDFFPSCDMRKDLRLALSVTETVAFSHCCINPLIYAFAGEKFRRYL---YHLYGKCL 312

```

RESULT 6

S68679

G protein-coupled receptor - human

C;Species: Homo sapiens (man)

C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

C;Accession: S68679

R;Stam, N.J.; Klomp, J.; van de Heuvel, M.; Olijve, W.

FEBS Lett. 384, 260-264, 1996

A;Title: Molecular cloning and characterization of a novel orphan receptor (P(2P)) expressed in human pancreas that shows high structural homology to the P(2U) purinoceptor.

A;Reference number: S68679; MUID:96197801; PMID:8617367

A;Accession: S68679
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-365 <STA>
 A;Cross-references: EMBL:X96597; NID:g1296631; PIDN:CAA65415.1; PID:g1296632
 C;Superfamily: ATP receptor P2u
 C;Keywords: G protein-coupled receptor

Query Match 21.3%; Score 352; DB 2; Length 365;
 Best Local Similarity 31.1%; Pred. No. 6e-22;
 Matches 90; Conservative 59; Mismatches 122; Indels 18; Gaps 6;

```

Qy      22 LSAFYAIEFIFGLLGNVTVVFYGYLEFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY-A 80
      |  ||: |: || |  :: ::| :: |:: |::|::||  :: :|| || | |
Db      38 LPVSYAVVFLGLGLNAPTLWLFI FRLRPWDATATYMFHLALSDTLYVLSLPTLIYYAA 97

Qy      81 NDKGTYGDVLCISNRYVLHTNLYTSILFLT FISM DRYLLMKYPFREHFLQKKEFAILISL 140
      ::  :| :|  |:: : ||| |: ||| ||: ||| : :| |  :  | | : |
Db      98 HNHWPFGTEICKFVRFLFYWNLYCSVLF L TCISVHRYLGICHPLRALRWGRPRLAGLLCL 157

Qy     141 AVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLSVMC 200
      ||| :|  ::| | |: :  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     158 AVWL VVAGCLVPNLFFVTTSNKGTTVLCHDTTRPEEFDHYVHFSSAVMGLLFGVPCIVTL 217

Qy     201 FFYYKMVFLKRR-----SQQQATALPLDKPQRLVVLAVVIFSILETPYHIMRNLRIA 253
      |  |  ||  |  |  :: |  :  |  :  :  :  :|:: | |::| | :
Db     218 VCYGLMA----RRLYQPLPGSAQSSSRL---RSLRTIAVVLTVFAVCFVFPFHITRTIYYL 270

Qy     254 SRLDSWPQGC-TQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
      :||  |  :  :| :||| | | :|: | | | | | |
Db     271 ARL--LEADCRVLNIVNVVYKVRPLASANSCLDPVLYLLTGDKYRRQL 317
  
```

RESULT 7

A57160

chemokine (C-C) receptor 4 - human

N;Alternate names: C-C CKR-4

C;Species: Homo sapiens (man)

C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000

C;Accession: A57160

R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; Wells, T.N.C.

J. Biol. Chem. 270, 19495-19500, 1995

A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor cDNA from a human basophilic cell line.

A;Reference number: A57160; MUID:95370289; PMID:7642634

A;Accession: A57160

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-360 <POW>

A;Cross-references: GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452

A;Note: source clone K5-5

C;Genetics:

A;Gene: GDB:CMKBR4

A;Cross-references: GDB:677463

A;Map position: 3p21-3p21

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F;40-65/Domain: transmembrane #status predicted <TM1>
 F;76-97/Domain: transmembrane #status predicted <TM2>
 F;112-133/Domain: transmembrane #status predicted <TM3>
 F;151-175/Domain: transmembrane #status predicted <TM4>
 F;208-226/Domain: transmembrane #status predicted <TM5>
 F;243-264/Domain: transmembrane #status predicted <TM6>
 F;291-308/Domain: transmembrane #status predicted <TM7>
 F;29-276,110-187/Disulfide bonds: #status predicted
 F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F;183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 20.4%; Score 336.5; DB 2; Length 360;
 Best Local Similarity 29.4%; Pred. No. 1.2e-20;
 Matches 93; Conservative 60; Mismatches 132; Indels 31; Gaps 9;

Qy	14	EAILNKYYL-----SAF-----YAIEFIFGLLGNTVVFGYLFCKMKNWN	52
		: : :: :	
Db	13	ESIYSNYYLYESIPKPCTKEGIKAFGELFLPPLYSLVFVFGLLGNSVVVL-VLFKYKRLR	71
Qy	53	S-SNVYLFNLSISDFAFLCTLPILIKSYANDKGTYGDLVCISNRYVLHTNLYTSILFLTF	111
		:: : : : : : :: : :	
Db	72	SMTDVYLLNLAISDLLFVFSLPFW-GYYAADQWVFGGLGCKMISWMYLVGFYSGIFFVML	130
Qy	112	ISMDRYLLMKYPFREHFLQKKEFAILISLAVWALVTLEVLPLMTFINSVPKEEGSNCIDY	171
		: : : : : : :: :: : :	
Db	131	MSIDRYLAIVHAVFSLRARTLTYGVITSLATWSVAVFASLPGFLESTCYTERNHTYCKTK	190
Qy	172	ASSGNPEHNLIYSLCLTLLGFLIPLSVMCFYYKMWVFLKRRSQQQATALPLDKPQRLVV	231
		: :: : : : : :: : : :::	
Db	191	YSLNSTTWKVLSSLEINILGLVIPLGIM-LFCYSMII----RTLQHCCKNEKKNKAVKMIF	245
Qy	232	LAVVIFSILFTPYHIMRNLRIRLDSWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFY	290
		: : : : : :: : : :	
Db	246	AVVVLFLGFWTPYNIVLFLETLELEVL-QDCTFERYLDAIQATETLAFVHCCLNPIIY	304
Qy	291	FLMGDHYREMLISKFR	306
		: : : : :: :	
Db	305	FFLGEKFRKYILQLFK	320

RESULT 8

I55450

G protein-coupled P2 receptor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 19-May-2000

C;Accession: I55450

R;Chang, K.; Hanaoka, K.; Kumada, M.; Takuwa, Y.

J. Biol. Chem. 270, 26152-26158, 1995

A;Title: Molecular cloning and functional analysis of a novel P2 nucleotide receptor.

A;Reference number: I55450; MUID:96064682; PMID:7592819
A;Accession: I55450
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <RES>
A;Cross-references: GB:D63665; NID:g1066007; PIDN:BAA09816.1; PID:g1066008
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor

Query Match 20.4%; Score 336; DB 2; Length 328;
Best Local Similarity 29.9%; Pred. No. 1.2e-20;
Matches 85; Conservative 52; Mismatches 137; Indels 10; Gaps 4;

```
Qy      22 LSAFYAIEFIFGLLGNVTVVFGYLCMKNNSSNVYLENLSISDFAFLCTLPILIKSYA- 80
      |  |:: : || || | :      :  | || |:::| : |::| | : ||
Db      29 LPPVYSVVLVVG LPLNVCVIAQICASRRITLRSVYTLNLALADLLYACSLPLLIYNYAR 88

Qy      81 NDKGTYGDVLCISNRYVLHTNLYTSILFLTIFISMDRYLLMKYPFRE-HFLQKKEFAILIS 139
      |  :||: |  |:: : ||: ||||| ||  ||| : :|  |  : | ::
Db      89 GDHWPFGLACRLVRFLFYANLHGSILFLTCISFQRYLGICHPLAPWHKRGRRRAAWVVC 148

Qy     140 LAVWALVTLEVL PMLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLSVM 199
      || :|| : ||  |  :  :  : | | :      | | : ||::||| : :
Db     149 GVVWLVTQAQCLPTAVFAATGIQRNRTVCYDLSPILSTRYLPYGMALTIVIGFLLPFTAL 208

Qy     200 CFFYYKMVFLKRRSQQQATALPL-----DKPQRLVVLAVVIFSILFTPYHIMRNLRIAS 254
      | :|  :| :|  | | :      | | : :| | | | :|| : :|
Db     209 LACYCRMA---RRLCRQDGPAGPVAQERRSKAARMAVVVAVFVISFLPFHITKTAYLAV 265

Qy     255 RLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYR 298
      |  :  : | || | || :|| : :  :|
Db     266 RSTPGVSCPVLETFAAAYKGTRPFASANSVLDPILEFYFTQQKFR 309
```

RESULT 9

A54946

P-2U nucleotide receptor - human

C;Species: Homo sapiens (man)

C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 17-Mar-1999

C;Accession: A54946

R;Parr, C.E.; Sullivan, D.M.; Paradiso, A.M.; Lazarowski, E.R.; Burch, L.H.;

Olsen, J.C.; Erb, L.; Weisman, G.A.; Boucher, R.C.; Turner, J.T.

Proc. Natl. Acad. Sci. U.S.A. 91, 3275-3279, 1994

A;Title: Cloning and expression of a human P-2U nucleotide receptor, a target for cystic fibrosis pharmacotherapy.

A;Reference number: A54946; MUID:94211846; PMID:8159738

A;Accession: A54946

A;Status: preliminary

A;Molecule type: mRNA; protein

A;Residues: 1-375 <PAR>

A;Cross-references: GB:U07225

A;Note: parts of this sequence were confirmed by protein sequencing

C;Genetics:

A;Gene: GDB:P2RY2; HP2U; P2U

A;Cross-references: GDB:362713; OMIM:600041

A;Map position: 11q13.5-11q14.1

C;Superfamily: ATP receptor P2u

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 20.3%; Score 335.5; DB 2; Length 375;
Best Local Similarity 33.1%; Pred. No. 1.5e-20;
Matches 93; Conservative 52; Mismatches 127; Indels 9; Gaps 7;

Qy 19 KY-YLSAFYAIEFIFGLLGNTVVFGYLFCKMKNWNSSNVYLFNLSISDFAFLCTLPILIK 77
|| | : : || | :: : | ||:| |:|:|:| : :|:|:
Db 32 KYVLLPVSYGVCVLGLCLNAVGLYIFLCRLKTWNASTTYMFHLAVSDALYAASLPLLVY 91

Qy 78 SYA-NDKGTYGDVLCISNRYVLHTNLYTSILFLTIFISMDRYLLMKYPFREHFLQKKEFAI 136
|| | : ||| |: : ||| ||||| ||: | | : | | : :|
Db 92 YYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTICISVHRCGLVLRPLRSLRWGRARYAR 151

Qy 137 LISLAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPL 196
:: ||| || |:| |: : : | | :: : || : | | :|
Db 152 RVAGAVWVLVLACQAPVLYFVTTTSARGP-LTCHDTSAPELFSRFVAYSSVMLGLLFAVPF 210

Qy 197 SVMCFFYYKMVFLKRRSQQQATALPLDKPQRLVVLAVV--IFSILFTPYHIMRNLRIAS 254
:|: | | | : : : || | : : :||| :|:| | |:| | | :
Db 211 AVILVCYVLMARRLLKPAYGTSGGLPRAKRKSVRTIAVVLAVFALCFLPFHVTRTLYYSF 270

Qy 255 RLDSWPQGC-TQKAIKSIYTLTRPLAFLNSAINPIFYFLMG 294
| | | | || | :|| || || ::|: ||| |
Db 271 R--SLDLSCHTLNAINMAYKVTR-LASANSCLDPVLYFLAG 308

RESULT 10

I50241

G protein-coupled receptor 6H1 - chicken

N;Alternate names: purinoceptor 6H1

C;Species: Gallus gallus (chicken)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 02-Jun-2000

C;Accession: I50241; JC4618

R;Kaplan, M.H.; Smith, D.I.; Sundick, R.S.

J. Immunol. 151, 628-636, 1993

A;Title: Identification of a G protein coupled receptor induced in activated T cells.

A;Reference number: I50241; MUID:93329058; PMID:8393036

A;Accession: I50241

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-308 <KAP>

A;Cross-references: GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:g304384

R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.

Biochem. Biophys. Res. Commun. 219, 105-110, 1996

A;Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.

A;Reference number: JC4618; MUID:96190677; PMID:8619790

A;Accession: JC4618

A;Molecule type: mRNA

A;Residues: 1-308 <WEB>

A;Cross-references: GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:g304384

A;Experimental source: T-cells

C;Comment: This receptor plays a role in T-cell activation.

C;Genetics:

A;Gene: p2Y5

C;Superfamily: ATP receptor P2u

C;Keywords: G protein-coupled receptor; transmembrane protein
 F;15-40/Domain: transmembrane #status predicted <TM1>
 F;51-74/Domain: transmembrane #status predicted <TM2>
 F;89-109/Domain: transmembrane #status predicted <TM3>
 F;133-153/Domain: transmembrane #status predicted <TM4>
 F;177-201/Domain: transmembrane #status predicted <TM5>
 F;227-248/Domain: transmembrane #status predicted <TM6>
 F;269-292/Domain: transmembrane #status predicted <TM7>

Query Match 20.2%; Score 333; DB 2; Length 308;
 Best Local Similarity 28.9%; Pred. No. 1.9e-20;
 Matches 88; Conservative 52; Mismatches 123; Indels 42; Gaps 6;

```

Qy      19 KYYL-SAFYAIEFIFGLLGNTVVFGYLFCKMKNWNSSNVYLFNLSISDFAFLCTLPILIK 77
      || |   ::: |: ||: |   :: : | :| | : |: ||: || | |: || | |
Db      13 KYTLYGCVFSMVFVLGLIANCVAIYIFTFLKVRNETTTYMLNLAISDLLFVFTLPFRIY 72

Qy      78 SYANDKGTYGDLVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAIL 137
      :      : |||| | : : : ||: | |||| | ||: ||: | : : || | : | :
Db      73 YFVVRNWPFGDVLCKISVTLFYTNMYGSILFLTCISVDRFLAIVHPFRSKTLRTRKNARI 132

Qy      138 ISLAVWALVTLEVLPLMTFFINSVPKEEGSNCIDYASSGNPEHNLIYSLC----- 186
      : : || | |      ||      : | | : : | |
Db      133 VCVAVWITVL-----AGSTPASFFQSTNRQNTEQRTCFENFPESTWKT 176

Qy      187 -----LTLLGFLIP--LSVMCFFYYKMVV-FLKRRSQQQATALPLDKPQRLVVLAVV 235
      : : : || || | : | |      ||: | : | | | : : : : : |
Db      177 YLSRIVIFIEIVGFFIPLILNVTC---STMVLRTLNKPPLTLNRNKLKSKKVLKMFVHLV 233

Qy      236 IFSILFTPYHIMRNLRIASRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFILMGD 295
      || | | ||: | | | : | | : : : | : | : | | : || | : |
Db      234 IFCFCFVPYNITLILYSIMRTQTWINCSVVTAVRTMYPVTLCIAVSNCCFDPIVYFTSD 293

Qy      296 HYREM 300
      | :
Db      294 TNSEL 298

```

RESULT 11

I58186

probable G protein-coupled receptor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000

C;Accession: I58186

R;Harrison, J.K.; Barber, C.M.; Lynch, K.R.

Neurosci. Lett. 169, 85-89, 1994

A;Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and brain related to chemokine receptors.

A;Reference number: I58186; MUID:94323113; PMID:8047298

A;Accession: I58186

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-354 <RES>

A;Cross-references: EMBL:U04808; NID:g2558635; PIDN:AAB87093.1; PID:g439861

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor

Query Match 20.2%; Score 332.5; DB 2; Length 354;
Best Local Similarity 27.9%; Pred. No. 2.5e-20;
Matches 82; Conservative 66; Mismatches 125; Indels 21; Gaps 6;

```
Qy      21 YLSAFYAIEFIFGLLGNVTVVFGYLFCKMKNWNSSNVYLFNLSISDFAFLCTLPILIKSYA 80
      :|| ||:: | |||:||: ||      |: : ::|| ||::|| |: |||
Db      34 FLSIFYSLVFTFGLVGNLLVVLALTNSRKSISITDIYLLNLALSDDLFFVATLPFWTHYLI 93

Qy      81 NDKGTYGDVLCISNRYVLHTNLYTSILFLTIFISMDRYLLMKYPFREHFLQKKEFAILISL 140
      : :| : : :|      : | |:| ||:|||| :      : : : |||
Db      94 SHEGLH-NAMCKLTTAFFFIGFFGGIFFITVISIDRYLAIVLAANSMMNRTVQHGVTSISL 152

Qy     141 AVWALVTLEVLPLMTFINSVPKEEGSNCI-DYASSGNPEHNLIYSLCLTLLGFLIPLSVM 199
      ||| | | | | : : |: ||      :: : : :|||::|| :|
Db     153 GVWAAAILVASPQFMF----TKRKDNECLGDYPEVLQEIWVPLRNSEVNILGFVLPLLIM 208

Qy     200 CFFYYKMV-VFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIASRLDS 258
      | |::|      ::::| |:      ||::| ||:| : :|||:|: |      :
Db     209 SFCYFRIVRTLFSCKNRKKARAI-----RLILLVVVVFFLFWTPYNIVIFLETCLKFYNF 262

Qy     259 WPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQYFKSL 312
      :|      :: : : :| :|| : :|| | | :      |||:| : |
Db     263 FPSCGMKRDLRWALSVTETVAFSHCCLNPFIIYAFAGE-----KFRRYLRLH 308
```

RESULT 12

JC4800

P2Y6 receptor - human

C;Species: Homo sapiens (man)

C;Date: 15-Oct-1995 #sequence_revision 16-Aug-1996 #text_change 17-Nov-2000

C;Accession: JC4800; G02514

R;Communi, D.; Parmentier, M.; Boeynaems, J.M.

Biochem. Biophys. Res. Commun. 222, 303-308, 1996

A;Title: Cloning, functional expression and tissue distribution of the human P2Y6 receptor.

A;Reference number: JC4800; MUID:96222498; PMID:8670200

A;Accession: JC4800

A;Molecule type: mRNA

A;Residues: 1-328 <COM>

A;Cross-references: EMBL:X97058

A;Experimental source: placenta

R;Hammet, F.; Southey, M.C.; Somers, G.R.; Hutchins, A.M.; Venter, D.J.
submitted to the EMBL Data Library, March 1996

A;Reference number: H01373

A;Accession: G02514

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 'M',4-328 <HAM>

A;Cross-references: EMBL:U52464; NID:g1407632; PIDN:AAB03572.1; PID:g1407633

C;Genetics:

A;Gene: P2Y6

C;Superfamily: ATP receptor P2u

C;Keywords: glycoprotein; placenta; receptor; transmembrane protein

F;26-52/Domain: transmembrane #status predicted <TMM1>

F;63-86/Domain: transmembrane #status predicted <TMM2>

F;104-122/Domain: transmembrane #status predicted <TMM3>

F;143-167/Domain: transmembrane #status predicted <TMM4>

F;193-216/Domain: transmembrane #status predicted <TMM5>
 F;241-264/Domain: transmembrane #status predicted <TMM6>
 F;283-305/Domain: transmembrane #status predicted <TMM7>
 F;5,173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 20.1%; Score 332; DB 2; Length 328;
 Best Local Similarity 30.6%; Pred. No. 2.5e-20;
 Matches 90; Conservative 48; Mismatches 136; Indels 20; Gaps 6;

```

QY      22 LSAFYAIEFIFGLLGNTVTVFGYLFCKMKNWNSSNVYLFNLSISDFAFLCTLPILIKSYA- 80
      |  | :  | | | : | :  :  : | | | | : | : | | : | |
Db      29 LPPVYSAVLAAGLPLNICVITQICTSRRALTRTAVYTLNLALADLLYACSLPLLIYNYAQ 88

QY      81 NDKGTYGDVLCISNRYVLHTNLYTSILFLTIFISMDRYLLMKYPFRE-HFLQKKEFAILIS 139
      |  : | | | : | : | | | | | | | | | : | : | : | | :
Db      89 GDHWPFQGFACRLVRFYANLHGSILFLTCISFQRYLGICHPLAPWHKRGGRRAAWLVC 148

QY     140 LAVWALVTLEVLPMPLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLSVM 199
      : | | | | | : | | | : : : | | : | : | : | | : | :
Db     149 VAVWLAVTTQCLPTAIFAATGIQRNRTVCYDLSPALATHYMPYGMALTIVIGFLLPFAAL 208

QY     200 CFFYYKMVFLKRRSQQQATALPL-----DKPQRLVVLAVVIFSILETPYHIMRNLRIAS 254
      | :  | : | | | :  | | : | : | : | : | : | : | :
Db     209 LACYCLLAC---RLCRQDGAEPVAQERRGKAARMAVVVAAFAISFLPFHITKTAYLAV 265

QY     255 RLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPI-FYFLMGDHYREMLISKFRQ 307
      |  : | : | | | | | : | | | | | | | | | : | :
Db     266 RSTPGVPCTVLEAFAAAAYKGRTPFASANSVLDPILFYFTQ-----KKFRR 310
  
```

RESULT 13

A45177

chemokine (C-C) receptor 1 - human

N;Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999

C;Accession: A45177; I55671

R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.

Cell 72, 415-425, 1993

A;Title: Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor.

A;Reference number: A45177; MUID:93161416; PMID:7679328

A;Accession: A45177

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-355 <NEO>

A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417

A;Experimental source: HL60 cells

A;Note: sequence extracted from NCBI backbone (NCBIP:124876)

R;Gao, J.

J. Exp. Med. 177, 1421-1427, 1993

A;Title: Structure and functional expression of the human macrophage inflammatory 1 alpha (MIP-1alpha)/RANTES receptor.

A;Reference number: I55671; MUID:93240122; PMID:7683036

A;Accession: I55671

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-355 <RES>
A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
C;Genetics:
A;Gene: GDB:CMKBR1; CMKR-1
A;Cross-references: GDB:138446; OMIM:601159
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F;36-60/Domain: transmembrane #status predicted <TM1>
F;71-91/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;147-171/Domain: transmembrane #status predicted <TM4>
F;205-223/Domain: transmembrane #status predicted <TM5>
F;240-264/Domain: transmembrane #status predicted <TM6>
F;288-305/Domain: transmembrane #status predicted <TM7>
F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;24-273,106-183/Disulfide bonds: #status predicted
F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 19.9%; Score 328; DB 2; Length 355;
Best Local Similarity 29.0%; Pred. No. 5.9e-20;
Matches 85; Conservative 63; Mismatches 127; Indels 18; Gaps 8;

```

Qy      22 LSAFYAIEFIFGLLGNVTVVFGYLFCKMKNWNSSNVYLFNLSISDFAFLCTLPLIKSYAN 81
      |  |:: |::|::|: |  :  : |::| |::| | | | |
Db      37 LPPLYSLVFVIGLVGNILVVLVLVQYKRLKNMTSIYLLNLAISDLLFLFTLPFWIDYK 96

Qy      82 DKGTYGDVLC--ISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILIS 139
      |  :| | :| | :| | | :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      97 DDWVFGDAMCKILSGFY--YTGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITS 154

Qy     140 LAVWALVTLEVLPMLTFINSVPKKEGSNC-IDYASSGNPEHNLIYSLCLTLLGFLIPLSV 198
      : :| | | | :| | | : : : | : : | | | | | :| | | :| | |
Db     155 IIIWALAILASMPGLYFSKTQWEEFTHHTCSLHFPHESLREWKLQALKLNLFGLVLP LLV 214

Qy     199 MCFYYKMOVFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIRASRLD- 257
      |  | :| :| | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     215 MIICYTGIKILLRRPNEKKS-----KAVRLIFVIMIIFFLFWTPYNL--TILISVFQDF 267

Qy     258 SWPQGCTQ-KAIKSIYTLTRELAFNLNSAINPIFYFLMGDHYREMLISKFRQYF 309
      :  | | : : :| :| : :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     268 LFTHCEQSRHLDLAVQVTEVIAYTHCCVNPVIYAFVGERFRKYL----RQLF 316

```

RESULT 14

JC4587

chemokine (C-C) receptor 4 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000

C;Accession: JC4587

R;Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996

A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to murine and human CC CKR-4.

A;Reference number: JC4587; MUID:96136324; PMID:8573157

A;Accession: JC4587
 A;Molecule type: mRNA
 A;Residues: 1-360 <HOO>
 A;Cross-references: EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852
 A;Experimental source: thymus
 C;Genetics:
 A;Gene: cc ckr-4
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: glycoprotein; phosphoprotein; receptor; thymus
 F;2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 19.8%; Score 326.5; DB 2; Length 360;
 Best Local Similarity 28.4%; Pred. No. 8e-20;
 Matches 93; Conservative 57; Mismatches 136; Indels 41; Gaps 10;

Qy	14	EAILNKYY-----LSAFYAIEFIFGLLGNVTVVFGYLCMKNNWN	52
		:	
Db	13	ETVYNSYYFYESMPKPCTKEGIKAFGEVFLPPLYSLVFLGLFGNSVVVL-VLFKYKRLK	71
Qy	53	S-SNVYLFNLSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTF	111
		:: : : : : : : :	
Db	72	SMTDVYLLNLAISDLLFVLSLPFW-GYYAADQWVFGGLCKIVSWMYLVGFYSGIFFIML	130
Qy	112	ISMDRYLLMKYPFREHFLQKKEFAILISLAVWALVTLEVLPM LTFINSVPKEEGSNCIDY	171
		: : : : : : : : : :	
Db	131	MSIDRYLAIVHAVFSLKARTLTYGVITSLITWSVAVFASLPGLLFSTCYTEHNHTYCKTQ	190
Qy	172	ASSGNPEHNLIYSLCLTLLGFLIPLSLVMCFYYKMWVFLKRRSQQQATALPLDKPQRLVV	231
		: : : : : : : : : :	
Db	191	YSVNSTTWKVLSSLEINV LGLLIPLGIM-LFWYSMII----RTLQHCCKNEKKNRAVRMIF	245
Qy	232	LAVVIFSILETPYHIMRNLRIRASRLDSWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFY	290
		: : ::: : : : : :	
Db	246	GVVVLFGLGFWTPYNVVLFLETLEVELEV-LQDCTLERYLDYAIQATETLGFHCCCLNPVIY	304
Qy	291	FLMGDHYREMLISKFRQYFKSLTSFRT	317
		: : :	
Db	305	FFLGE-----KFRKYITQL--FRT	321

RESULT 15

JN0605

somatostatin receptor 4 - human

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000

C;Accession: JN0605; JN0762; A47457

R;Xu, Y.; Song, J.; Bruno, J.F.; Berelowitz, M.

Biochem. Biophys. Res. Commun. 193, 648-652, 1993

A;Title: Molecular cloning and sequencing of a human somatostatin receptor, hSSTR4.

A;Reference number: JN0605; MUID:93290656; PMID:8512564

A;Accession: JN0605
 A;Molecule type: DNA
 A;Residues: 1-388 <XUY>
 A;Cross-references: GB:L14856; NID:g292499; PIDN:AAA36623.1; PID:g292500
 R;Yamada, Y.; Kagimoto, S.; Kubota, A.; Yasuda, K.; Masuda, K.; Someya, Y.;
 Ihara, Y.; Li, Q.; Imura, H.; Seino, S.; Seino, Y.
 Biochem. Biophys. Res. Commun. 195, 844-852, 1993
 A;Title: Cloning, functional expression and pharmacological characterization of
 a fourth (hSSTR4) and a fifth (hSSTR5) human somatostatin receptor subtype.
 A;Reference number: JN0762; MUID:93384611; PMID:8373420
 A;Accession: JN0762
 A;Molecule type: DNA
 A;Residues: 1-388 <YAM>
 A;Cross-references: GB:D16826; NID:g693907; PIDN:BAA04106.1; PID:g693908
 R;Rohrer, L.; Raulf, F.; Bruns, C.; Buettner, R.; Hofstaedter, F.; Schule, R.
 Proc. Natl. Acad. Sci. U.S.A. 90, 4196-4200, 1993
 A;Title: Cloning and characterization of a fourth human somatostatin receptor.
 A;Reference number: A47457; MUID:93248256; PMID:8483934
 A;Accession: A47457
 A;Molecule type: DNA
 A;Residues: 1-82, 'T', 84-364, 'K', 366-388 <ROH>
 A;Cross-references: GB:L07833; NID:g307429; PIDN:AAA60565.1; PID:g307430
 A;Note: sequence extracted from NCBI backbone (NCBIN:130856, NCBIP:130858)
 C;Comment: This protein mediates the diverse actions of the tetradecapeptide
 somatostatin.
 C;Genetics:
 A;Gene: GDB:SSTR4
 A;Cross-references: GDB:202662; OMIM:182454
 A;Map position: 20p11.2-20p11.2
 A;Introns: #status absent
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor;
 lipoprotein; phosphoprotein; thiolester bond; transmembrane protein
 F;47-73/Domain: transmembrane #status predicted <TM1>
 F;84-109/Domain: transmembrane #status predicted <TM2>
 F;121-142/Domain: transmembrane #status predicted <TM3>
 F;162-184/Domain: transmembrane #status predicted <TM4>
 F;208-238/Domain: transmembrane #status predicted <TM5>
 F;257-284/Domain: transmembrane #status predicted <TM6>
 F;291-314/Domain: transmembrane #status predicted <TM7>
 F;24/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;119-198/Disulfide bonds: #status predicted
 F;161,253/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase)
 #status predicted
 F;327/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 19.7%; Score 325.5; DB 2; Length 388;
 Best Local Similarity 28.4%; Pred. No. 1.1e-19;
 Matches 82; Conservative 66; Mismatches 110; Indels 31; Gaps 5;

Qy	22	LSAFYAIEFIFGLLGNVTVVFGYLCMKNNWSSNVYLFNLSISDFAFLCTLPILIKSYAN	81
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Db	50	IQCIYALVCLVGLVGNALVIFVILRYAKMKTATNIYLLNLAVADELFMLSVPFVASSAAL	109
Qy	82	DKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILISLA	141
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Qy	142	VWALVTLEVLPM	TFINSVPKEEGS	NCIDYASSGNPEHN	LIYSLCLTLLGFLIPLSVMCF	201
			:	: :	: : : :	:
Db	170	VWLASLLVTLPIA	IFADTRPARGGQ	AVACNLQWPHPAWS	AVFVVYTFLLGFLLPVLAIGL	229
Qy	202	FYYKMV-----	VFL-----	KRRSQQQATALPLDKP	QRLVVLAVVIFSILETPYHIMRNL	250
		:		: : :	: : : : : : : :	
Db	230	CYLLIVGKMRAVAL	RAGWQQRRRSEK	KIT-----	RLVLMVVVVFVLCWMPFYVVQLL	281
Qy	251	R-IASRLDSWPQGCT	QKAIKSIYTLTRPLAFLNS	SAINPIFYFLMGDHYR		298
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Db	282	NLVVTSLDA-----	TVNHVSLILSYAN	SCANPILYGFLSDNFR		319

Search completed: August 23, 2004, 17:03:36
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 23, 2004, 17:03:00 ; Search time 125 Seconds
(without alignments)
796.951 Million cell updates/sec

Title: US-09-891-138A-2
Perfect score: 1650
Sequence: 1 MAQNLSCENWLATEAILNKY.....REMLISKFRQYFKSLTSFRT 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1295152 seqs, 314255058 residues

Total number of hits satisfying chosen parameters: 1295152

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	ID	Description

1	1650	100.0	317	10	US-09-891-138A-2	Sequence 2, Appli
2	1238.5	75.1	330	14	US-10-225-567A-567	Sequence 567, App
3	1238.5	75.1	334	10	US-09-764-886-45	Sequence 45, Appl
4	1238.5	75.1	334	10	US-09-764-886-70	Sequence 70, Appl
5	1238.5	75.1	334	12	US-09-764-886-45	Sequence 45, Appl
6	1238.5	75.1	334	12	US-09-764-886-70	Sequence 70, Appl
7	1238.5	75.1	334	12	US-09-875-076-36	Sequence 36, Appl
8	1238.5	75.1	334	12	US-09-876-252-38	Sequence 38, Appl
9	1238.5	75.1	334	14	US-10-272-983-36	Sequence 36, Appl
10	1238.5	75.1	334	14	US-10-393-807-36	Sequence 36, Appl
11	1238.5	75.1	334	15	US-10-417-820A-38	Sequence 38, Appl
12	1238.5	75.1	334	15	US-10-264-237-2757	Sequence 2757, Ap
13	1238.5	75.1	334	16	US-10-723-955-38	Sequence 38, Appl
14	1238.5	75.1	334	16	US-10-782-596-36	Sequence 36, Appl
15	1238.5	75.1	379	12	US-10-311-671-3	Sequence 3, Appli
16	1231.5	74.6	334	9	US-09-765-034-2	Sequence 2, Appli
17	1226.5	74.3	334	16	US-10-706-532-2	Sequence 2, Appli
18	1224.5	74.2	334	14	US-10-270-587-2	Sequence 2, Appli
19	1141.5	69.2	288	10	US-09-764-886-80	Sequence 80, Appl
20	1141.5	69.2	288	12	US-09-764-886-80	Sequence 80, Appl
21	479	29.0	289	10	US-09-764-886-79	Sequence 79, Appl
22	479	29.0	289	12	US-09-764-886-79	Sequence 79, Appl
23	479	29.0	373	10	US-09-991-225-5	Sequence 5, Appli
24	479	29.0	373	12	US-10-369-405-5	Sequence 5, Appli
25	479	29.0	373	12	US-10-375-157-6	Sequence 6, Appli
26	479	29.0	373	14	US-10-092-135-7	Sequence 7, Appli
27	479	29.0	373	14	US-10-010-568-6	Sequence 6, Appli
28	479	29.0	373	15	US-10-023-634-60	Sequence 60, Appl
29	475	28.8	299	14	US-10-270-144-4	Sequence 4, Appli
30	475	28.8	373	12	US-10-375-157-5	Sequence 5, Appli
31	475	28.8	373	14	US-10-010-568-5	Sequence 5, Appli
32	475	28.8	373	15	US-10-023-634-58	Sequence 58, Appl
33	475	28.8	373	16	US-10-055-569A-50	Sequence 50, Appl
34	474	28.7	373	10	US-09-745-842-14	Sequence 14, Appl
35	474	28.7	373	12	US-10-344-728-6	Sequence 6, Appli
36	474	28.7	373	12	US-10-375-157-7	Sequence 7, Appli
37	474	28.7	373	12	US-10-375-157-8	Sequence 8, Appli
38	474	28.7	373	14	US-10-092-135-5	Sequence 5, Appli
39	474	28.7	373	14	US-10-092-135-6	Sequence 6, Appli
40	474	28.7	373	14	US-10-225-567A-219	Sequence 219, App
41	474	28.7	373	14	US-10-010-568-7	Sequence 7, Appli
42	474	28.7	373	14	US-10-010-568-8	Sequence 8, Appli
43	474	28.7	373	15	US-10-023-634-59	Sequence 59, Appl
44	474	28.7	373	15	US-10-023-634-61	Sequence 61, Appl
45	474	28.7	373	16	US-10-055-569A-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1
 US-09-891-138A-2
 ; Sequence 2, Application US/09891138A
 ; Publication No. US20030083245A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lin, Daniel Chi-Hong

```
; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030083245A1e1 Receptors
; FILE REFERENCE: 018781-006210US
; CURRENT APPLICATION NUMBER: US/09/891,138A
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,461
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: mouse TGR18 G-protein coupled receptor (GPCR)
US-09-891-138A-2
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Query Match          100.0%; Score 1650; DB 10; Length 317;
Best Local Similarity 100.0%; Pred. No. 4.6e-142;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy     61 LSISDFAFLCTLPILIKSYANDKGTYGVDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LSISDFAFLCTLPILIKSYANDKGTYGVDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120

Qy    121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHN 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHN 180

Qy    181 LIYSLCLTLLGFLIPLSVMCFFYYKMVFLKRRSQQATALPLDKPQRLVVLAVVIFSIL 240
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Db    181 LIYSLCLTLLGFLIPLSVMCFFYYKMVFLKRRSQQATALPLDKPQRLVVLAVVIFSIL 240

Qy    241 FTPYHIMRNLRIASRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREM 300
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Db    241 FTPYHIMRNLRIASRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREM 300

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RESULT 2

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US-10-225-567A-567
; Sequence 567, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
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; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED
RECEPTORS (GPCRS)
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 567
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-567
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Query Match          75.1%; Score 1238.5; DB 14; Length 330;
Best Local Similarity 72.2%; Pred. No. 1.5e-104;
Matches 228; Conservative 42; Mismatches 45; Indels 1; Gaps 1;
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Db    121 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 180

Qy    181 LIYSLCLTLLGFLIPLSVMCFYYKMMVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
      ||||:| ||||| ||||| |||||:|:|:|:|:| |||||:| ||:|:| |||||:|
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Qy    241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
      |||||:|:|:| ||||| || | ||| | | | :| ||||| |||:|:|:|:|:|:|:|:|
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RESULT 3

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US-09-764-886-45
; Sequence 45, Application US/09764886
; Publication No. US20030139327A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ02
; CURRENT APPLICATION NUMBER: US/09/764,886
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 88
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-886-45

Query Match 75.1%; Score 1238.5; DB 10; Length 334;
Best Local Similarity 72.2%; Pred. No. 1.5e-104;
Matches 228; Conservative 42; Mismatches 45; Indels 1; Gaps 1;

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Db      5 MAWNATCKNWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLEN 64

Qy     61 LSI SDF AFLCTLPILIKSYANDKGT YGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
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Db     65 LSVSDL AFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

Qy    121 KYPFREHFLQKKEFAILISLAWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHN 180
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Qy    181 LIYSLCLTLLGFLIPLSVMCFFYYKMVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
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Qy    241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
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RESULT 4

US-09-764-886-70

; Sequence 70, Application US/09764886
; Publication No. US20030139327A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ02
; CURRENT APPLICATION NUMBER: US/09/764,886
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-886-70

Query Match 75.1%; Score 1238.5; DB 10; Length 334;
Best Local Similarity 72.2%; Pred. No. 1.5e-104;

Matches 228; Conservative 42; Mismatches 45; Indels 1; Gaps 1;

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Db      5 MAWNATCKNWLAAEAALAKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLEN 64

Qy     61 LSISDFAFLCTLPILIKSYANDKGTYGDLVCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
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Qy    121 KYPFREHFLQKKEFAILISLAWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHN 180
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Db    125 KYPFREHLLQKKEFAILISLAIWVLVTLELLPLPLINPVITDNGTTCNDFASSGDPNYN 184

Qy    181 LIYSLCLTLLGFLIPLSVMCFFYYKMVFLKRRSQQQATAPLDKPQRLVVLAVVIFSIL 240
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Db    185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATAPLEKPLNLVIMAVVIFSIL 244

Qy    241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
      ||||:|:|:| || | | | | | | | | | | | | | | | | | | | | | |
Db    245 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 304

Qy    300 MLISKFRQYFKSLTSF 315
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Db    305 MLMNQLRHNFKSLTSF 320

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RESULT 5

US-09-764-886-45

; Sequence 45, Application US/09764886

; Publication No. US20020086822A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PTZ02

; CURRENT APPLICATION NUMBER: US/09/764,886

; CURRENT FILING DATE: 2001-01-17

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 88

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 45

; LENGTH: 334

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-764-886-45

Query Match 75.1%; Score 1238.5; DB 12; Length 334;
 Best Local Similarity 72.2%; Pred. No. 1.5e-104;
 Matches 228; Conservative 42; Mismatches 45; Indels 1; Gaps 1;

```

Qy      1 MAQNLSCEWLATEAILNKYYLSAFYAIEFIFGLLGNTVVFGYLFCKMKNWNSSNVYLEN 60
      || | :|:|||| || | |||| | |||: |:|| | |:|:| :|:||||:||||
Db      5 MAWNATCKNWLAAEAALAKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLEN 64

Qy     61 LSISDFAFLCTLPILIKSYANDKGTYGDLVCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
      ||:| | |||||:|:|:| | ||||| ||||| ||||| |||||:|:|:|
Db     65 LSVSDLAFCTLPLMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

```

Qy 121 KYPFREHFLQKKEFAILISLAWWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHN 180
 ||||| :|||:|:| | | : | :|||:| :|
 Db 125 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 184

Qy 181 LIYSLCLTLLGFLIPLSVMCFFYYKMVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
 |||:||||| :|||:|:| | | :|||:| :|||:|
 Db 185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSIL 244

Qy 241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
 |||:|:|:| | | | | :|||:| | :|||:| :|
 Db 245 FTPYHVMRNVRIASRLGSWKYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 304

Qy 300 MLISKFRQYFKSLTSF 315
 ||:: | |||||
 Db 305 MLMNQLRHNFKSLTSF 320

RESULT 6

US-09-764-886-70

; Sequence 70, Application US/09764886

; Publication No. US20020086822A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PTZ02

; CURRENT APPLICATION NUMBER: US/09/764,886

; CURRENT FILING DATE: 2001-01-17

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 88

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 70

; LENGTH: 334

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-764-886-70

Query Match 75.1%; Score 1238.5; DB 12; Length 334;
 Best Local Similarity 72.2%; Pred. No. 1.5e-104;
 Matches 228; Conservative 42; Mismatches 45; Indels 1; Gaps 1;

Qy 1 MAQNLSCEWNLATEAILNKYYLSAFYAIEFIFGLLGNTVVFGYLCMKNNSSNVYLEN 60
 || | :|:|||| || | |||| || |||: |:|| | |:||:| :|||:|:|
 Db 5 MAWNATCKNWLAEEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLEN 64

Qy 61 LSISDFAFLCTLPLIKSYANDKGTYGDLVCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
 ||:| | |||||:|:| || | ||||| |||||:|:|:|
 Db 65 LSVSDLAFCTLPLMIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

Qy 121 KYPFREHFLQKKEFAILISLAWWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHN 180
 ||||| :|||:|:| | | : | :|||:| :|
 Db 125 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 184

Qy 181 LIYSLCLTLLGFLIPLSVMCFFYYKMVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
 |||:||||| :|||:|:| | | :|||:| :|||:|
 Db 185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSIL 244

Qy 241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
 ||||:||||:||||| || | ||| | | :||||||| |||:||||:||||:
 Db 245 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 304

Qy 300 MLISKFRQYFKSLTSF 315
 ||:: | |||||
 Db 305 MLMNQLRHNFKSLTSF 320

RESULT 7

US-09-875-076-36

; Sequence 36, Application US/09875076
 ; Publication No. US20030017528A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Ruoping
 ; APPLICANT: Dang, Huong T.
 ; APPLICANT: Liaw, Chen W.
 ; APPLICANT: Lin, I-Lin
 ; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
 ; FILE REFERENCE: AREN0050
 ; CURRENT APPLICATION NUMBER: US/09/875,076
 ; CURRENT FILING DATE: 2001-06-06
 ; PRIOR APPLICATION NUMBER: 09/417,044
 ; PRIOR FILING DATE: 1999-10-12
 ; PRIOR APPLICATION NUMBER: 60/120,416
 ; PRIOR FILING DATE: 1999-02-16
 ; PRIOR APPLICATION NUMBER: 60/121,851
 ; PRIOR FILING DATE: 1999-02-26
 ; PRIOR APPLICATION NUMBER: 60/123,946
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/123,949
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/136,436
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/136,437
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/136,439
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/136,567
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/137,127
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/137,131
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/141,448
 ; PRIOR FILING DATE: 1999-06-29
 ; PRIOR APPLICATION NUMBER: 60/156,653
 ; PRIOR FILING DATE: 1999-09-29
 ; PRIOR APPLICATION NUMBER: 60/156,633
 ; PRIOR FILING DATE: 1999-09-29
 ; PRIOR APPLICATION NUMBER: 60/156,555
 ; PRIOR FILING DATE: 1999-09-29
 ; PRIOR APPLICATION NUMBER: 60/156,634
 ; PRIOR FILING DATE: 1999-09-29
 ; PRIOR APPLICATION NUMBER: 60/157,280
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: 60/157,294


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; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
;   LENGTH: 334
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-875-076-36
```

RESULT 8

; TITLE OF INVENTION: Non-Endogenous Constitively Activated Human G Protein
Coupled Receptors
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01

; PRIOR APPLICATION NUMBER: 60/157,294
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: 60/157,281
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: 60/157,282
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: 60/156,633
 ; PRIOR FILING DATE: 1999-09-29
 ; NUMBER OF SEQ ID NOS: 146
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 38
 ; LENGTH: 334
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-876-252-38

Query Match 75.1%; Score 1238.5; DB 12; Length 334;
 Best Local Similarity 72.2%; Pred. No. 1.5e-104;
 Matches 228; Conservative 42; Mismatches 45; Indels 1; Gaps 1;

Qy	1	MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCKMKNWNSSNVYLFN	60
		: : : : : :	
Db	5	MAWNATCKNWLAEEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN	64
Qy	61	LSISDFAFLCTLPLIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM	120
		: : : : : :	
Db	65	LSVSDLAFCTLPLMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII	124
Qy	121	KYPFREHFLQKKEFAILISLAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHN	180
		: : : : : :	
Db	125	KYPFREHLLQKKEFAILISLAIWVLVTLELLPLPLINPVITDNGTTCNDFASSGDPNYN	184
Qy	181	LIYSLCLTLLGFLIPLSVMCFFYYKMVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL	240
		: : : : :	
Db	185	LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL	244
Qy	241	FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE	299
		: : : :	
Db	245	FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD	304
Qy	300	MLISKFRQYFKSLTSF	315
		: : :	
Db	305	MLMNQLRHNFKSLTSF	320

RESULT 9

US-10-272-983-36

; Sequence 36, Application US/10272983
 ; Publication No. US20030148450A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Ruoping
 ; APPLICANT: Dang, Huong T.
 ; APPLICANT: Liaw, Chen W.
 ; APPLICANT: Lin, I-Lin
 ; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
 ; FILE REFERENCE: AREN0050
 ; CURRENT APPLICATION NUMBER: US/10/272,983

```

; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-983-36

```

```

Query Match          75.1%; Score 1238.5; DB 14; Length 334;
Best Local Similarity 72.2%; Pred. No. 1.5e-104;
Matches 228; Conservative 42; Mismatches 45; Indels 1; Gaps 1;

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Qy      1 MAQNLSCEWNLATEAILNKYYLSAFYAIEFIFGLLGNTVVVFGYLFCKMKNWNSSNVYLFN 60
      || | :||| || | |||| || ||| :||| ||:||| :||| ||||
Db      5 MAWNATCKNWLAAEALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 64

Qy     61 LSISDFAFLCTLPILIKSYANDKGTYGDLVCISNRYVLHTNLYTSILFLTFISMDDRYLLM 120
      ||:|| ||||| :||:|||| ||||| ||||| ||||| ||||| :||| :
Db     65 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

Qy    121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHN 180
      ||||| ||||| ||||| :| ||||:||:| || | : | :| |||:| :|
Db    125 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 184

Qy    181 LIYSLCLTLLGFLIPLSVMCFFYYKMVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
      |||:||||| ||||| :|||:|:| |||||:| ||:|||||:|
Db    185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL 244

Qy    241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
      ||||:||||:||||| || | || | :| ||||| |||:||||:|:|
Db    245 FTPYHVMRNVRIASRLGSWKQYQCTQVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 304

Qy    300 MLISKFRQYFKSLTSF 315
      ||:: | |||||
Db    305 MLMNQLRHNEFKSLTSF 320

```

RESULT 10
 US-10-393-807-36
 ; Sequence 36, Application US/10393807
 ; Publication No. US20030175891A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Ruoping
 ; APPLICANT: Dang, Huong T.
 ; APPLICANT: Liaw, Chen W.
 ; APPLICANT: Lin, I-Lin
 ; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
 ; FILE REFERENCE: AREN0050
 ; CURRENT APPLICATION NUMBER: US/10/393,807
 ; CURRENT FILING DATE: 2003-03-21
 ; PRIOR APPLICATION NUMBER: US/09/417,044
 ; PRIOR FILING DATE: 1999-10-12
 ; PRIOR APPLICATION NUMBER: 60/109,213
 ; PRIOR FILING DATE: 1998-11-20
 ; PRIOR APPLICATION NUMBER: 60/120,416
 ; PRIOR FILING DATE: 1999-02-16
 ; PRIOR APPLICATION NUMBER: 60/121,851
 ; PRIOR FILING DATE: 1999-02-26
 ; PRIOR APPLICATION NUMBER: 60/123,946
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/123,949
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/136,436
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/136,437
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/136,439
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/136,567
 ; PRIOR FILING DATE: 1999-05-28
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 74
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 36
 ; LENGTH: 334
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-393-807-36

Query Match 75.1%; Score 1238.5; DB 14; Length 334;
 Best Local Similarity 72.2%; Pred. No. 1.5e-104;
 Matches 228; Conservative 42; Mismatches 45; Indels 1; Gaps 1;

QY	1	MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNTVVVFGYLFCKMKNWNSSNVYLFN	60
		: : : : : : : : :	
Db	5	MAWNATCKNWLAAEAALKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN	64
QY	61	LSISDFAFLCTLPLIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM	120
		: : : : : : : :	
Db	65	LSVSDLAFLCTLPLMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII	124
QY	121	KYPFREHFLQKKEFAILISLAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHN	180

Db	125	KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN	184
Qy	181	LIYSLCLTLLGFLIPLSVMCFFYYKMVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL	240
Db	185	LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSIL	244
Qy	241	FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE	299
Db	245	FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD	304
Qy	300	MLISKFRQYFKSLTSF	315
Db	305	MLMNQLRHNFKSLTSF	320

RESULT 11

US-10-417-820A-38

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; Sequence 38, Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: 7.US28.CON
; CURRENT APPLICATION NUMBER: US/10/417,820A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 334
; TYPE: PRT

```

```

Query Match          75.1%; Score 1238.5; DB 15; Length 334;
Best Local Similarity 72.2%; Pred. No. 1.5e-104;
Matches 228; Conservative 42; Mismatches 45; Indels 1; Gaps 1;

Qy      1 MAQNLSCEWNLATEAILNKYYLSAFYAIEFIFGLLGNTVVFVGYLFCMKNWNSSNVYLFN 60
      || | :||| || | |||| || ||| :|| ||:||| :||| |||
Db      5 MAWNATCKNWLAAEAALKEYYSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 64

Qy     61 LSISDFAFLCTLPLILIKSYANDKGYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
      ||:|| |||||:|:|||| ||||| ||||| ||||| |||||:|:|:|
Db     65 LSVSDLAFLLCTLPLMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

Qy    121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHN 180
      ||||| ||||| |||||:| |||||:| || | :|:| |:| |||:| :|
Db    125 KYPFREHLLQKKEFAILISLAIWVLVTLELLPLPLINPVITDNGTTCNDFASSGDPNYN 184

Qy    181 LIYSLCLTLLGFLIPLSVMCFFYYKMVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
      |||:| ||||| ||||| :|:|:|:| |||||:| ||:| |||||:|
Db    185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL 244

Qy    241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
      ||||:|:|:| || | || | || | :||| ||||| ||:| |||:|:|:|
Db    245 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 304

Qy    300 MLISKFRQYFKSLTSF 315
      ||::| | |||||
Db    305 MLMNOLRHNFKSLTSF 320

```

Query Match 75.1%; Score 1238.5; DB 15; Length 334;
Best Local Similarity 72.2%; Pred. No. 1.5e-104;
Matches 228; Conservative 42; Mismatches 45; Indels 1; Gaps 1;


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; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/782,596
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US/09/875,076
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-782-596-36

```

```

Query Match          75.1%; Score 1238.5; DB 16; Length 334;
Best Local Similarity 72.2%; Pred. No. 1.5e-104;
Matches 228; Conservative 42; Mismatches 45; Indels 1; Gaps 1;

```

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Qy      1 MAQNLSCEWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCKMKNWNSSNVYLEN 60
      || | :|:|||| || | ||||| || |||: |:||| ||:||:| :|||||:||||
Db      5 MAWNATCKNWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLEN 64

Qy     61 LSISDFAFLCTLPLILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
      ||:|| |||||:|:|:|||| ||||| ||||| |||||:|:|:|:
Db     65 LSVSDLAFLCTLPLMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

Qy    121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHN 180
      ||||| ||||| |||||:| |||||:|:| || | : |: | |:|:|:| :|
Db    125 KYPFREHLLQKKEFAILISLAIWVLVTLELLPLPLINPVITDNGTTCNDFASSGDPNYN 184

Qy    181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
      |||:|:|:|:|:| |||||:|:|:|:|:| |||||:| ||:|:|:|:|
Db    185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL 244

Qy    241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
      |||||:|:|:|:| || | || | || | || | || | || | || | || | || |
Db    245 FTPYHVMRNVRIASRLGSKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 304

Qy    300 MLISKFRQYFKSLTSF 315

```

Db ||::: | |||||
305 MLMNQLRHNFKSLTSF 320

RESULT 15

US-10-311-671-3

; Sequence 3, Application US/10311671
; Publication No. US20040072996A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: LAL, Preeti G.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: HAFALIA, April J. A.
; APPLICANT: NGUYEN, Danniel B.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: KALLICK, Deborah A.
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: YUE, Henry
; APPLICANT: KHAN, Farrah A.
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: LU, Yan
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: GRAUL, Richard
; APPLICANT: YAO, Monique G.
; APPLICANT: YANG, Junming
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: AU-YOUNG, Janice K.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: HERNANDEZ, Roberto
; APPLICANT: WALSH, Roderick T.
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: THORNTON, Michael B.
; APPLICANT: HE, Ann
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0131 USN
; CURRENT APPLICATION NUMBER: US/10/311,671
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/19275
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,483
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/213,954
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/215,209
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 60/216,595
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,936
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/219,154
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/220,141
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PERL Program

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; SEQ ID NO 3
;   LENGTH: 379
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 3485895CD1
US-10-311-671-3
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Query Match          75.1%;   Score 1238.5;   DB 12;   Length 379;
Best Local Similarity 72.2%;   Pred. No. 1.8e-104;
Matches 228;   Conservative 42;   Mismatches 45;   Indels 1;   Gaps 1;
```

```
QY      1 MAQNLSCEWNLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCKMKNWNSSNVYLFN 60
      || | :|:|||| || | |||| || |||: |:||| ||:|:| :|:||||:||||
Db      50 MAWNATCKNWLAEEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 109

QY      61 LSISDFAFLCTLPLIKSYANDKGTYGDLVCISNRYVLHTNLYTSILFLTIFISMDRYLLM 120
      ||:| | |||||:|:|:| || | ||||| ||||| |||||:|:|:|:|
Db      110 LSVSDLAFLLCTLPLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTIFISIDRYLII 169

QY      121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHN 180
      ||||| ||||| |||||:| ||||:|:| || | : |: | |:|:|:| :|
Db      170 KYPFREHLLQKKEFAILISLAIWVLVTLELLPLPLINPVITDNGTTCNDFASSGDPNYN 229

QY      181 LIYSLCLTLLGFLIPLSVMCFFYYKMVFLKRRSQQATALPLDKPQRLVVLAVVIFSIL 240
      |||:|:|:|:|:| |||||:| :|:|:|:| |||||:| ||:|:|:|:|
Db      230 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSIL 289

QY      241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
      ||||:|:|:|:| || | || | | | :|:|:|:| ||:|:|:|:|:|
Db      290 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 349

QY      300 MLISKFRQYFKSLTSF 315
      ||::: | |||||
Db      350 MLMNQLRHNFKSLTSF 365
```

```
Search completed: August 23, 2004, 17:14:30
Job time : 127 secs
```

OM protein - protein search, using sw model

Run on: August 23, 2004, 16:55:03 ; Search time 115 Seconds
(without alignments)
869.733 Million cell updates/sec

Title: US-09-891-138A-2
Perfect score: 1650
Sequence: 1 MAQNLSCEWNLATEAILNKY.....REMLISKFRQYFKSLTSFRT 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score Match Length DB ID	Description

1	1634	99.0	317	11	Q99MT6	Q99mt6 mus musculu
2	1238.5	75.1	330	4	Q9BXA5	Q9bxa5 homo sapien
3	1238.5	75.1	334	4	Q8TDQ8	Q8tdq8 homo sapien
4	482.5	29.2	361	13	Q90X57	Q90x57 xenopus lae
5	479	29.0	373	11	Q8BMJ5	Q8bmj5 mus musculu
6	461	27.9	357	13	Q9DE05	Q9de05 raja erinac
7	422.5	25.6	374	13	O57466	O57466 meleagris g
8	416	25.2	347	13	Q7ZZA4	Q7zza4 brachydanio
9	386.5	23.4	537	13	Q7ZWQ7	Q7zwq7 xenopus lae
10	353	21.4	361	11	Q8VHP3	Q8vhp3 cavia porce
11	343	20.8	360	6	Q8MJW8	Q8mjlw8 canis famil
12	338	20.5	328	11	Q9ERK9	Q9erk9 mus musculu
13	335	20.3	355	6	Q9MYJ8	Q9myj8 callithrix
14	333	20.2	355	11	Q9JLY8	Q9jly8 rattus norv
15	328	19.9	374	4	Q86VA9	Q86va9 homo sapien
16	326.5	19.8	354	11	Q8CBJ0	Q8cbj0 mus musculu
17	326	19.8	351	6	Q9MYJ9	Q9myj9 oryctolagus
18	325.5	19.7	354	11	Q8BR50	Q8br50 mus musculu
19	323.5	19.6	360	11	Q91ZH4	Q91zh4 rattus norv
20	319	19.3	332	13	Q7T0X4	Q7t0x4 xenopus lae
21	319	19.3	344	4	Q7Z3S6	Q7z3s6 homo sapien
22	318.5	19.3	309	11	Q8R528	Q8r528 mus musculu
23	317.5	19.2	355	6	Q8HZN7	Q8hzn7 gorilla gor
24	316.5	19.2	355	6	Q95LH1	Q95lhl1 macaca fasc
25	316.5	19.2	385	11	Q8BQ97	Q8bq97 mus musculu
26	316	19.2	367	13	Q9PVG0	Q9pvg0 carassius a
27	316	19.2	370	13	Q8QFR6	Q8qfr6 xenopus lae
28	315	19.1	355	4	Q9BYX5	Q9byx5 homo sapien
29	314	19.0	344	4	Q7Z3S0	Q7z3s0 homo sapien
30	313	19.0	355	11	Q8BVW4	Q8bvw4 mus musculu
31	313	19.0	355	11	Q8BMH9	Q8bmh9 mus musculu
32	313	19.0	367	13	Q9PVF9	Q9pvf9 carassius a
33	312.5	18.9	355	4	Q8IUZ1	Q8iuz1 homo sapien
34	312.5	18.9	355	6	Q8HZN8	Q8hzn8 pan troglod
35	312.5	18.9	390	13	Q8QGQ4	Q8qqq4 carassius a
36	310.5	18.8	339	4	Q8N5S7	Q8n5s7 homo sapien
37	310	18.8	370	11	Q8BKK1	Q8bkk1 mus musculu
38	309.5	18.8	355	6	Q8HZN3	Q8hzn3 papio hamad
39	308.5	18.7	355	6	Q8HZN4	Q8hzn4 cercopithec
40	308.5	18.7	357	11	Q7TMV7	Q7tmv7 mus musculu
41	308.5	18.7	390	11	Q7TT86	Q7tt86 rattus norv
42	307.5	18.6	390	13	Q8AXM7	Q8axm7 carassius a
43	307	18.6	362	4	Q8NE10	Q8nel0 homo sapien
44	307	18.6	375	11	Q8BYI1	Q8byi1 mus musculu
45	306.5	18.6	355	6	Q8HZN6	Q8hzn6 pongo pygma

ALIGNMENTS

RESULT 1

Q99MT6

ID Q99MT6 PRELIMINARY; PRT; 317 AA.

AC Q99MT6;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE G-protein coupled receptor GPR91.
 GN GPR91.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL;
 RX MEDLINE=21172992; PubMed=11273702;
 RA Wittenberger T., Schaller H.C., Hellebrand S.;
 RT "An expressed sequence tag (est) data mining strategy succeeding in
 RT the discovery of new g-protein coupled receptors.";
 RL J. Mol. Biol. 307:799-813(2001).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AF295367; AAK01867.1; -.
 DR MGD; MGI:1934135; Gpr91.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 317 AA; 36701 MW; 4E22F0608F928E36 CRC64;

Query Match 99.0%; Score 1634; DB 11; Length 317;
 Best Local Similarity 99.1%; Pred. No. 8.8e-133;
 Matches 314; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MAQNLSCE	NWLATEA	ILNKYYLS	AFYAIEFI	FGLLGNVT	VVFGYLF	CMKNWNSS	NNVYLFN	60
Db	1	MAQNLSCE	NWLATEA	ILNKYYLS	AFYAIEFI	FGLLGNVT	VVFGYLF	CMKNWNSS	NNVYLFN	60
Qy	61	LSISDFA	FLCTLP	ILIKSYAN	DKGTYGD	VLCISNRY	VLHTNL	YTSILFL	TFISMDR	YLLM 120
Db	61	LSISDFA	FLCTLP	ILIKSYAN	DKGTYGD	VLCISNRY	VLHTNL	YTSMLLL	TVISMDR	YLLM 120
Qy	121	KYPFREH	FLQKKE	FAILISL	AVWALVT	LEVLPML	TFINSVP	KKEEGSN	CIDYASS	GNPEHN 180
Db	121	KYPFREH	FLQKKE	FAILISL	AVWALVT	LEVLPML	TFINSVP	KKEEGSN	CIDYASS	GNPEHN 180
Qy	181	LIYSLCL	TLLGFL	IPLSVMC	FFYYKM	VVFLKRR	SQQQATA	PLDKPQ	RLVVLAV	VIFSIL 240
Db	181	LIYSLCL	TLLGFL	IPLSVMC	FFYYKM	VVFLKRR	SQQQATA	PLDKPQ	RLVVLAV	VIFSIL 240
Qy	241	FTPYHIM	RNLRIAS	RLDSPQG	CTQKA	IKSIYTL	TRPLAFL	NSAINPI	IFYFLMG	DHYREM 300
Db	241	FTPYHIM	RNLRIAS	RLDSPQG	CTQKA	IKSIYTL	TRPLAFL	NSAINPI	IFYFLMG	DHYREM 300
Qy	301	LISKFRQ	YFKSLT	SFRT						
Db	301	LISKFRQ	YFKSLT	SFRT						

RESULT 2

Q9BXA5

ID Q9BXA5 PRELIMINARY; PRT; 330 AA.
AC Q9BXA5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE G-protein coupled receptor 91.
GN GPR91.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21172992; PubMed=11273702;
RA Wittenberger T., Schaller H.C., Hellebrand S.;
RT "An expressed sequence tag (est) data mining strategy succeeding in
RT the discovery of new g-protein coupled receptors.";
RL J. Mol. Biol. 307:799-813(2001).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF348078; AAK29080.1; -.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0016526; F:G-protein coupled receptor activity, unknow. . .; NAS.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 330 AA; 38283 MW; 6D3C70E340866BAB CRC64;

Query Match 75.1%; Score 1238.5; DB 4; Length 330;
Best Local Similarity 72.2%; Pred. No. 1.1e-98;
Matches 228; Conservative 42; Mismatches 45; Indels 1; Gaps 1;

Qy 1 MAQNLSCEWNLATEAILNKYYLSAFYAIEFIFGLLGNTVTVVFGYLFCKMKNWNSSNVYLFN 60
| | | : | | | | | | | | | | | | | : | : | | | | | : | | | | | | | |
Db 1 MAWNATCKNWLAAEALEKYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 60
Qy 61 LSISDFAFLCTLPILIKSYANDKGTYGDLVCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
| : | | | | | | | : | : | | | | | | | | | | | | | | | : | | | : |
Db 61 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 120
Qy 121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHN 180
| | | | | | | | | | | | | : | | | | : | : | | | : | : | : | : | : |
Db 121 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 180
Qy 181 LIYSLCLTLLGFLIPLSVMCFYYKMMVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
| | | : | | | | | | | | | | | : | : | : | : | : | | | | | : | : | : |
Db 181 LIYSMCLTLLGFLIPLFVMCFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSIL 240
Qy 241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
| | | : | : | : | | | | | | | | | : | | | | | | | : | : | : | : | : |

Db 241 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 300
 Qy 300 MLISKFRQYFKSLTSF 315
 ||::: | |||||
 Db 301 MLMNQLRHNFKSLTSF 316

RESULT 3

Q8TDQ8

ID Q8TDQ8 PRELIMINARY; PRT; 334 AA.
 AC Q8TDQ8;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE P2Y purinoceptor 1 (G protein-coupled receptor 91).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang W., Li N., Wan T., Cao X.;
 RT "Human P2Y purinoceptor 1.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AF247785; AAL95690.1; -.
 DR EMBL; BC030948; AAH30948.1; -.
 DR Genew; HGNC:4542; GPR91.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 334 AA; 38697 MW; 33146E1AD87F0E81 CRC64;

Query Match 75.1%; Score 1238.5; DB 4; Length 334;
 Best Local Similarity 72.2%; Pred. No. 1.1e-98;
 Matches 228; Conservative 42; Mismatches 45; Indels 1; Gaps 1;

Qy 1 MAQNLSCEWNLATEAILNKYYLSAFYAIEFIFGLLGNTVVFGYLFCKMKNWNSSNVYLFN 60
 || | :||| || | |||| || ||| :||| ||::||| :|||::|||
 Db 5 MAWNATCKNWLAAEALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 64
 Qy 61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
 ||::|| |||||::||:|||| ||||| ||||| |||||::|||::
 Db 65 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

Qy	121	KYPFREHFLQKKEFAILISLAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHN	180
Db	125	KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN	184
Qy	181	LIYSLCLTLLGGLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL	240
Db	185	LIYSMCLTLLGGLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL	244
Qy	241	FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE	299
Db	245	FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD	304
Qy	300	MLISKFRQYFKSLTSF	315
Db	305	MLMNQLRHNEFKSLTSF	320

Q90X57

```

ID      Q90X57          PRELIMINARY;          PRT;   361 AA.
AC      Q90X57;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      P2Y1 nucleotide receptor.
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipioidea; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCBI_TaxID=8355;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Cheng A.W., Tsim K.W.;
RT      "Cloning of Xenopus P2Y1 Receptor.";
RL      Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF432354; AAL27614.1; -.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0004872; F:receptor activity; IEA.
DR      GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR      GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR      InterPro; IPR000276; GPCR_Rhodpsn.
DR      Pfam; PF00001; 7tm_1; 1.
DR      PRINTS; PR00237; GPCRRHODOPSN.
DR      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR      PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW      Receptor.
SQ      SEQUENCE      361 AA;  41002 MW;  E5B2D605F5B57FED CRC64;

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Query Match 29.2%; Score 482.5; DB 13; Length 361;
Best Local Similarity 36.7%; Pred. No. 1.6e-33;
Matches 114; Conservative 58; Mismatches 124; Indels 15; Gaps 8;

QY 1 MAQNLSCEWNLATEAILNK-----YYLSAFYAIEFIFGLLGNVTVVFGYLFCKMKNWNSSN 55
: | | | : | | | | | : | | : | : : | | : | :
Db 18 LASGSSAGN--VTKCSLTKTGFQFYLLPAVYIVVCITGFIGNSVAIWMFIHMKPWSSIS 75

Qy 56 VYLFNLSISDFAFLCTLPILIKSYANDKG-TYGDVLCISNRYVLHTNLYTSILFLTISM 114
 ||:||||::|| :::|| || || :|| || |::| ||| ||||| ||:
 Db 76 VYMFNLALADFLYVLSLPALIFYFYFNKTDWIFGDALCKLQRFHFVNLYGSILFLTICISV 135

Qy 115 DRYLLMKYPFREHFLQKKEFAILISLAVWALVTLEVLPMPLTFINS-VPKEEGSNCIDYAS 173
 || : :| : ||: :| || || :| : |:| | : : | : || :|
 Db 136 HRYTGVVHPLKSLGRLKKNSIYISALVWFIVIAGISPILFFSGTGIRKNKTITCFDTSS 195

Qy 174 SGNPEHNLIYSLCLTLLGFLIPLSVMCFFYYKMVFLKRRSQQQATALPLDKPQ-RLVVL 232
 |||:| |: || || :: | :| | : | || | ||::
 Db 196 DEYLRSYFIYSMCTTVFGFCIPFILILGCYGLIVRALIYKDMNNA---PLRKKSIVLVII 252

Qy 233 AVVIFSILFTPYHIMRNLRIASRLD-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFY 290
 : :|:: : |:|:|:| : :|| | : | : :| :|| || ||| :|||
 Db 253 VLTVFAVSYPFHVMMKNLNLRLRDLDFQSPMECNFNDRVYATYQVTRGLASLNSCVDPILY 312

Qy 291 FLMGDHYREML 301
 || || :| |
 Db 313 FLAGDTFRRKL 323

RESULT 5

Q8BMJ5

ID Q8BMJ5 PRELIMINARY; PRT; 373 AA.
 AC Q8BMJ5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE P2Y purinoceptor 1.
 GN P2RY1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL; AK030759; BAC27125.1; -.
 DR MGD; MGI:105049; P2ry1.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 SQ SEQUENCE 373 AA; 42228 MW; BA88124B7847287C CRC64;

Query Match 29.0%; Score 479; DB 11; Length 373;
 Best Local Similarity 37.6%; Pred. No. 3.2e-33;

Matches 108; Conservative 54; Mismatches 117; Indels 8; Gaps 7;

```
Qy      20 YYLSAFYAIEFIFGLLGNTVVFGYLFCKMKNWNSSNVYLFNLSISDFAFLCTLPIILIKSY 79
      ||| | | : || | |||  :: |:| || | : :||:||||::|| :: ||| || |
Db      52 YYLPAVYILVFIIGFLGNSVAIWVYVFMKPPWGSISVYMFNLALADFLYVLTLPALIFYY 111

Qy      80 ANDKG-TYGDVLCISNRYVLHTNLTYTSILFLTIFISMDRYLLMKYPFREFHFLQKKEFAILI 138
      |      :|| :|  |:: | ||| ||||| ||  || : || :  ||: || :
Db     112 FNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTICISAHRYSGVVYPLKSLGRLKKKNAIYV 171

Qy     139 SLAVWALVTLEVLPMPLTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
      |: || :| : : |:| : :  | :  | | | :  |||:| |: | |||
Db     172 SVLVWLIVVVAISPILFYSGTGRKNKTVTCTYD'TTSNDYLRSYFIYSMCTTVAMFCIPL- 230

Qy     198 VMCFFYYKMVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL 256
      |:  | :|| |  || | ||:: : |:| : |:|:| : : :|
Db     231 VLILGCYGLIV--KALIYNDLNSPLRRKSIYLVIIIVLTVEAVSYIPFHVMTMNLRLARL 288

Qy     257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
      |  |: |  : : | :|| || ||| :|| ||| || :| |
Db     289 DFQTPMCDNFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335
```

RESULT 6

Q9DE05

```
ID   Q9DE05      PRELIMINARY;      PRT;    357 AA.
AC   Q9DE05;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   P2Y receptor.
OS   Raja erinacea (Little skate).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Squalia; Hypnosqualea; Pristiorajae; Batoidea;
OC   Rajiformes; Rajidae; Raja.
OX   NCBI_TaxID=7782;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20459151; PubMed=10900200;
RA   Dranoff J.A., O'Neill A.F., Franco A.M., Cai S.Y., Connolly G.C.,
RA   Ballatori N., Boyer J.L., Nathanson M.H.;
RT   "A primitive ATP receptor from the little skate Raja erinacea.";
RL   J. Biol. Chem. 275:30701-30706(2000).
DR   EMBL; AF242850; AAG42684.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE    357 AA;  41239 MW;  14604EE15DCBDB41 CRC64;
```

Query Match 27.9%; Score 461; DB 13; Length 357;
Best Local Similarity 35.0%; Pred. No. 1.1e-31;
Matches 110; Conservative 64; Mismatches 112; Indels 28; Gaps 11;

QY	17	LNK----	YYLSAFYAIEFIFGLLGNVTVVFGYLF	FCMKNNWNSSNVYLFNLSISDFAFLCTL	72
				: : : : : : : : : :	
Db	29	LNKGFQFYYPIMYIIVFVTGFIGNSVALWMFI	FHMRPWSSITIYMFNLVLADLFYVFSL	88	
QY	73	PILIKSYANDKG-TYGDVLCISNRYVLHTNLYTS	SILFLTFISMDRYLLMKYPF	131	
			: : : : : : : :		
Db	89	PILIFYFENKTDWIFGELLCKLXRFI	FHVNLVYGSILFLTCISVHRYTG	148	
QY	132	KEFAILISLAVWALVTLEVLPLMTFINS	-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLL	190	
		: : : : : : : : :			
Db	149	KKSATIVCVCVWITVMAGISPILYFSRTGLRRNKTNT	CYDTTSKELLETYFIYSMSTTFF	208	
QY	191	GFLIPLS--VMCF-FYYKMVVF	LKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIM	247	
		: : : : : : : : : :			
Db	209	GFCIPFATILVCYGFIVKALI-----	SNDMKTPL-RGKSVRLVIIVLAVFAISYLPFHVM	262	
QY	248	RNLRIASRLDSWPQG---CT-QKAIKSIYTLTRPLAFLNS	AINPIFYFLMGDHYREMLIS	303	
		: : : : : : : : :			
Db	263	KNLNLQSRSL--YYQGLDTC	EWNRRVYATYQVTRGLASLNSCVDPIYFLAGDTFR-----	315	
QY	304	KFRQYFKSLT	SFRT	317	
		: : :			
Db	316	--RRFTNAASREMT	327		

RESULT 7

```

OS7466
ID 057466 PRELIMINARY; PRT; 374 AA.
AC 057466;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE G protein coupled P2Y nucleotide receptor.
GN TP2Y.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=98086419; PubMed=9415702;
RA Boyer J.L., Waldo G.L., Harden T.K.;
RT "Molecular cloning and expression of an avian G protein-coupled P2Y
RT receptor.";
RL Mol. Pharmacol. 52:928-934(1997).
DR EMBL; AF031897; AAC60339.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.

```


DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 347 AA; 39861 MW; 3D3C01F83CC283E2 CRC64;

Query Match 25.2%; Score 416; DB 13; Length 347;
 Best Local Similarity 35.7%; Pred. No. 8.1e-28;
 Matches 105; Conservative 57; Mismatches 116; Indels 16; Gaps 9;

QY 19 KY-YLSAFYAIEFIFGLLGNTVVFGYLFCKMKNWNSSNVYLFNLSISDFAFLCTLPILIK 77
 || | |:: ||: | :: :: | : | | |::|::| :: :||:|
 Db 19 KYILLPVSYSLVCFGLILNSVALWMFITKMRPWKPSTVYMFHLALSDTLYVLSLPLMIY 78
 QY 78 SYAN-DKGTYGDLVLCISNRYVLHTNLYTSILFLTIFISMDRYLLMKYPFREHFLQKKEFAI 136
 ||| :| ||| |:: : ||| ||||| ||: ||| : :| | | |
 Db 79 YYANRSHWPFGVVLCKIVRFLFYANLYCSILFLTICISVHRYLGICHPIRSLTLIKPRHAH 138
 QY 137 LISLAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPE--HNLI-YSLCLTLLGFL 193
 :: || | ::| | ::| : | | : || || : | : :| |:
 Db 139 MVCGFVWTAVIACLVPTLILVNTSRNGNSTLCHD---TSRPEEFHNFVTYNSVVMVLLFI 195
 QY 194 IPLSVMCFFYYKMVVF-----KRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRN 249
 :| | : | | | :| | :: | :|:: :|:| | | |::| |
 Db 196 LPFLVIVVCYCLMARALCQPRKGLAQNQSS-SRKKSIIKLIIVVLVFAICFVPFHITRT 254
 QY 250 LRIASRLDSWPQGC-TQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLI 302
 | | | : : | | : | :||| :|| :|| ||| |||| |:
 Db 255 LYYAYRI--FDADCKTLNIVNFSYKITRPLASVNSCLDPILYFLAGDHYRSKLL 306

RESULT 9

Q7ZWQ7

ID Q7ZWQ7 PRELIMINARY; PRT; 537 AA.
 AC Q7ZWQ7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC046837; AAH46837.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.

RL J. Pharmacol. Exp. Ther. 297:43-49(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF298899; AAG24619.1; -.
 DR EMBL; BC027331; AAH27331.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Hypothetical protein; Receptor.
 SQ SEQUENCE 328 AA; 36721 MW; 00F9DF5ADADF903E CRC64;

Query Match 20.5%; Score 338; DB 11; Length 328;
 Best Local Similarity 29.6%; Pred. No. 4e-21;
 Matches 84; Conservative 54; Mismatches 136; Indels 10; Gaps 4;

Qy	22	LSAFYAIEFIFGLLGNVTVVFGYLFCKMKNWNSSNVYLFNLSISDFAFLCTLPILIKSYA-	80
		: : : : : ::: : : : :	
Db	29	LTPVYSVVLVGLPLNICVIAQICASRRTLTRSAVYTLNLALADLMYACSLPLLIYNYAR	88
Qy	81	NDKGTYGDLVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPPRE-HFLQKKEFAILIS	139
		: : :: : : : : : : :	
Db	89	GDHWPFGLACRFVRFYANLHGSILFLTCISFQRYLGICHPLASWHKRGRRAAWVVC	148
Qy	140	LAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLSVM	199
		: : : : : : : :	
Db	149	GVVWLAVTAQCLPTAVFAATGIQRNRTVCYDLSPILSTRYLPYGMALTIVIGFLLPFIAL	208
Qy	200	CFFYKMWVFLKRRSQQQATALPL-----DKPQRLVVLAVVIFSILETPYHIMRNLRIAS	254
		: : : : : : : : :	
Db	209	LACYCRMA---RRLCRQDGPAGPVAQERRSKAARMVVVAVFAISFLPFHITKTAYLAV	265
Qy	255	RLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYR	298
		: : : : : : :	
Db	266	RSTPGVSCPVLETFAAAYKGRPFASVNSVLDPIIFYFTQQKFR	309

RESULT 13

Q9MYJ8

ID Q9MYJ8 PRELIMINARY; PRT; 355 AA.

AC Q9MYJ8;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Chemokine receptor.

GN CCR1.

OS Callithrix jacchus (Common marmoset).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.

OX NCBI_TaxID=9483;

RN [1]


```

DE    Macrophage inflammatory protein-1 alpha receptor.
OS    Rattus norvegicus (Rat).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX    NCBI_TaxID=10116;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    STRAIN=CD;
RX    MEDLINE=20555330; PubMed=11091494;
RA    Waller A., Nayee P., Czaplowski L.G.;
RT    "Identification and characterization of a rat macrophage inflammatory
RT    protein-1 alpha receptor.";
RL    J. Hematother. Stem Cell Res. 9:703-710(2000).
DR    EMBL; AF119381; AAF34340.1; -.
DR    GO; GO:0016021; C:integral to membrane; IEA.
DR    GO; GO:0004872; F:receptor activity; IEA.
DR    GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR    GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR    InterPro; IPR000276; GPCR_Rhodpsn.
DR    Pfam; PF00001; 7tm_1; 1.
DR    PRINTS; PR00237; GPCRRHODOPSN.
DR    PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR    PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW    Receptor.
SQ    SEQUENCE    355 AA;  40838 MW;  2FEB8661D1E6E075 CRC64;

```

Qy	22	LSAFYAEIEFIFGLLGNVTVVFGYLFCEMKNNWSSNVYLFNLISDFAFLCTLPILIKSYAN	81
Db	37	LPPLYSFVFTIIGVVGNIILVILVLMQHRRLQSMTSIYLFNLAVSDLVFLFTLPFWIDYKLL	96
Qy	82	DKGTYGDVLC--ISNRYVLHTNLYTSILFLTIFISMDRYLLMKYPFREHFLQKKEFAILIS	139
Db	97	DNWVFGDAMCKLLSGFYLL--GLYSEIFFIILLTIDRYLAIVHAVFSLRARTVTFGIITS	154
Qy	140	LAVWALVTLEVLPMLTFINSVKPEEGSNCIDYASSGNPEHNL-----IYSLCLTLLGFLI	194
Db	155	IIIWALAILASIPALCFKQWFEFTHHTC----SPHFPDES�KTWKRFQALKNLNLGLIL	210
Qy	195	PLSVMCFFYYKMV-VFLKRRSQQQATALPLDKPQRLVVLAVVIFSILEFTPYHIMRNLR	253
Db	211	PLLVMIIICYAGIIRILLRRPNEKKAKAV-----RLIFAITLFFLLWTPYNL--TVFVS	262
Qy	254	SRLD-SWPQGCTQ-KAISKIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQY	308
Db	263	AFQDVLFTNQCEQSKQLDLAIQVTEVIAYTHCCVNPIIYVFVGERFRKYLRQLFRH	319

Db	116	DDWVFGDAMCKILSGFY--YTGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITS	173
Qy	140	LAVWALVTLEVLPMPLTFINSVPKEEGSNC-IDYASSGNPEHNLIYSLCLTLLGFLIPLSV	198
Db	174	IIIWALAILASMPGLYFSKTQWEFTHHTCSLHFPHESLREWKLQALKNLFGVLPLLV	233
Qy	199	MCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSILEFTPYHIMRNLRIASRLD-	257
Db	234	MIICYTGIIKILLRRPNEKKS-----KAVRLIFVIMIIFFLFWTPYNL--TILISVFQDF	286
Qy	258	SWPQGCTQ-KAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQYF	309
Db	287	LFTHECEQSRHLDLAVQVTEVIAYTHCCVNPVIYAFVGERFRKYL---RQLF	335

Search completed: August 23, 2004, 17:02:52
Job time : 119 secs

OM protein - protein search, using sw model

Run on: August 23, 2004, 16:47:58 ; Search time 25 Seconds
 (without alignments)
 660.250 Million cell updates/sec

Title: US-09-891-138A-2
 Perfect score: 1650
 Sequence: 1 MAQNLSCEWNLATEAILNKY.....REMLISKFRQYFKSLTSFRT 317

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	DB	ID	Description
No.						
1	481	29.2	373	1	P2YR_CAVPO	P59902 cavia porce
2	479	29.0	373	1	P2YR_RAT	P49651 rattus norv
3	475	28.8	373	1	P2YR_MOUSE	P49650 mus musculu
4	474	28.7	373	1	P2YR_BOVIN	P48042 bos taurus
5	474	28.7	373	1	P2YR_HUMAN	P47900 homo sapien
6	472.5	28.6	362	1	P2YR_CHICK	P34996 gallus gall
7	472.5	28.6	362	1	P2YR_MELGA	P49652 meleagris g
8	426	25.8	337	1	GP80_HUMAN	Q96p68 homo sapien
9	386.5	23.4	537	1	P2Y8_XENLA	P79928 xenopus lae
10	379.5	23.0	328	1	P2Y3_CHICK	Q98907 gallus gall
11	374	22.7	374	1	P2Y2_RAT	P41232 rattus norv
12	373.5	22.6	373	1	P2Y2_MOUSE	P35383 mus musculu
13	371.5	22.5	328	1	P2Y3_MELGA	O93361 meleagris g
14	363.5	22.0	377	1	P2Y2_HUMAN	P41231 homo sapien
15	354	21.5	361	1	P2Y4_RAT	O35811 rattus norv
16	353	21.4	355	1	C3X1_HUMAN	P49238 homo sapien
17	352	21.3	365	1	P2Y4_HUMAN	P51582 homo sapien

18	343	20.8	361	1	P2Y4_MOUSE	Q9jjs7	mus musculu
19	336.5	20.4	360	1	CKR4_HUMAN	P51679	homo sapien
20	336	20.4	328	1	P2Y6_RAT	Q63371	rattus norv
21	333	20.2	308	1	P2Y5_CHICK	P32250	gallus gall
22	332.5	20.2	354	1	C3X1_RAT	P35411	rattus norv
23	332	20.1	328	1	P2Y6_HUMAN	Q15077	homo sapien
24	329	19.9	355	1	CKR1_MACMU	P56482	macaca mula
25	328	19.9	355	1	CKR1_HUMAN	P32246	homo sapien
26	326.5	19.8	346	1	CLT2_HUMAN	Q9ns75	homo sapien
27	326.5	19.8	360	1	CKR4_MOUSE	P51680	mus musculu
28	325.5	19.7	354	1	C3X1_MOUSE	Q9z0d9	mus musculu
29	325.5	19.7	388	1	SSR4_HUMAN	P31391	homo sapien
30	321	19.5	344	1	P2Y5_MOUSE	Q8bmc0	mus musculu
31	319.5	19.4	345	1	CLT2_PIG	Q95n03	sus scrofa
32	319	19.3	353	1	APJ_XENLA	P79960	xenopus lae
33	318.5	19.3	359	1	IL8B_MOUSE	P35343	mus musculu
34	317.5	19.2	355	1	GPR1_HUMAN	P46091	homo sapien
35	317	19.2	368	1	SSR2_BOVIN	P34993	bos taurus
36	316.5	19.2	384	1	SSR4_RAT	P30937	rattus norv
37	315.5	19.1	355	1	GPR1_MACMU	O97664	macaca mula
38	315.5	19.1	355	1	IL8A_RABIT	P21109	oryctolagus
39	315	19.1	355	1	CKR8_HUMAN	P51685	homo sapien
40	314	19.0	344	1	P2Y5_HUMAN	P43657	homo sapien
41	314	19.0	369	1	SSR2_HUMAN	P30874	homo sapien
42	314	19.0	369	1	SSR2_PIG	P34994	sus scrofa
43	314	19.0	370	1	P2Y9_HUMAN	Q99677	homo sapien
44	313.5	19.0	353	1	IL8B_PANTR	Q28807	pan troglod
45	313.5	19.0	356	1	CKR8_MACMU	O97665	macaca mula

ALIGNMENTS

RESULT 1

P2YR_CAVPO

ID P2YR_CAVPO STANDARD; PRT; 373 AA.
AC P59902;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
GN P2RY1.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Small intestine;
RA Gao N., Hu H., Zhu M.X., Wood J.D.;
RT "A novel P2Y1 receptor in the guinea pig submucous plexus.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC !- FUNCTION: Receptor for extracellular adenine nucleotides such as
CC ATP and ADP (By similarity).
CC !- SUBCELLULAR LOCATION: Integral membrane protein.
CC !- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----

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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; AY048684; AAL05953.1; -.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 57 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 58 78 1 (POTENTIAL).
 FT DOMAIN 79 89 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 90 110 2 (POTENTIAL).
 FT DOMAIN 111 128 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 129 149 3 (POTENTIAL).
 FT DOMAIN 150 167 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 168 188 4 (POTENTIAL).
 FT DOMAIN 189 220 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 221 241 5 (POTENTIAL).
 FT DOMAIN 242 258 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 259 279 6 (POTENTIAL).
 FT DOMAIN 280 310 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 311 331 7 (POTENTIAL).
 FT DOMAIN 332 373 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 124 202 BY SIMILARITY.
 FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 373 AA; 42300 MW; 2BD66543FFE3F341 CRC64;

Query Match 29.2%; Score 481; DB 1; Length 373;
 Best Local Similarity 36.9%; Pred. No. 1.1e-24;
 Matches 106; Conservative 58; Mismatches 115; Indels 8; Gaps 6;

Qy 20 YYLSAFYAIEFIFGLLGNVTVVFGLFCMKNWNSSNVYLENLSISDFAFLCTLPILIKSY 79
 ||| | : || | ||| :: ::| || | : ||:||||::|| :: ||| || |
 Db 52 YYLPAVYIVVFIIGFLGNSIAIWMVFVHMKPWSGISVYMFNLALADFLYVLTLPALIFY 111
 Qy 80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILI 138
 | :|| :| |:: | ||| ||||| || || : || : ||: | : |
 Db 112 FNKTNWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNVYI 171
 Qy 139 SLAVWALVTLEVLPLMTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
 |: || :| : : |:| : : : | : | | | ||:| |: | :||
 Db 172 SVLVWLIVVVAISPILFYSGTGIRKNKTITCYDTSDEYLRSYFIYSMCTTVAMFCVPLV 231
 Qy 198 VMCFYYKVVFLKRRSQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIRASRL 256
 :: | :| | : : || | ||:: : :||: : |:|:| : : :||
 Db 232 LILGCYGLIVRALIYKDLDNS---PLRRKSIYLVIIIVLTVFAVSYIPFHVMTMNLRLARL 288
 Qy 257 D-SWPQGCT-QKAIKSIYTLRPLAFLNSAINPIFYFLMGDHYREML 301
 | |: || : : | :|| || ||| ::|| ||| || :| |
 Db 289 DFQTPMCTFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335

RESULT 2

P2YR_RAT

ID P2YR_RAT STANDARD; PRT; 373 AA.
AC P49651;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
GN P2RY1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Insulinoma;
RX MEDLINE=95298025; PubMed=7779087;
RA Tokuyama Y., Hara M., Jones E.M.C., Fan Z., Bell G.I.;
RT "Cloning of rat and mouse P2Y purinoceptors."
RL Biochem. Biophys. Res. Commun. 211:211-218(1995).
CC -!- FUNCTION: Receptor for extracellular adenine nucleotides such as
CC ATP and ADP. In pancreatic islets, may mediate some of the effects
CC of extracellular ATP on insulin secretion.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in muscle, heart, liver, kidney,
CC lung, brain, spleen, but not in testis.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
DR EMBL; U22830; AAA91303.1; -.
DR HSSP; P34996; 1DDD.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 52 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 53 74 1 (POTENTIAL).
FT DOMAIN 75 87 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 88 109 2 (POTENTIAL).
FT DOMAIN 110 126 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 127 147 3 (POTENTIAL).
FT DOMAIN 148 166 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 167 188 4 (POTENTIAL).
FT DOMAIN 189 218 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 219 238 5 (POTENTIAL).
FT DOMAIN 239 265 CYTOPLASMIC (POTENTIAL).

FT	TRANSMEM	266	285	6 (POTENTIAL).
FT	DOMAIN	286	303	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	304	328	7 (POTENTIAL).
FT	DOMAIN	329	373	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	124	202	BY SIMILARITY.
FT	CARBOHYD	11	11	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	27	27	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	113	113	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	197	197	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	373 AA;	42321 MW;	6DDF676287B5E648 CRC64;

Query Match 29.0%; Score 479; DB 1; Length 373;
 Best Local Similarity 37.3%; Pred. No. 1.5e-24;
 Matches 107; Conservative 57; Mismatches 115; Indels 8; Gaps 6;

Qy	20	YYLSAFYAIEFIFGLLGNVTVVFGYLFCKMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY	79
		: :: :: : : :: :	
Db	52	YYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFY	111
Qy	80	ANDKG-TYGDVLCISNRYVLHTNLNLYTSILFLTFSMDRYLLMKYPFREHFLQKKEFAILI	138
		: : : : : : :	
Db	112	FNKTDWIFGDMCKLQRFIFHVNLGYSILFLTCSAHRYSGVVYPLKSLGRLKKKNAIYV	171
Qy	139	SLAVWALVTLEVLPLMTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS	197
		: : : : : : : : : :	
Db	172	SVLVWLIVVVAISPILFYSGTGIRKNKTVTCTDSTSDEYLRSYFIYSMCTTVAMFCIPLV	231
Qy	198	VMCFFYYKMVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL	256
		:: : : : :: : : :: : :: : : :	
Db	232	LILGCYGLIVRALIYKDLNS---PLRRKSIYLVIIVLTVFAVSYIPFHVMTMNLRLARL	288
Qy	257	D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML	301
		: : : : : :	
Db	289	DFQTPMCDNFNDRVYATYQVTRGLASLNSCVDPIYFLAGDTFRRL	335

RESULT 3

P2YR_MOUSE

ID P2YR_MOUSE STANDARD; PRT; 373 AA.
 AC P49650;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
 GN P2RY1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Insulinoma;
 RX MEDLINE=95298025; PubMed=7779087;
 RA Tokuyama Y., Hara M., Jones E.M.C., Fan Z., Bell G.I.;
 RT "Cloning of rat and mouse P2Y purinoceptors."
 RL Biochem. Biophys. Res. Commun. 211:211-218(1995).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv;
 RA Leon C.;
 RT "Thromboresistance in P2Y1 receptor knockout mice.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Receptor for extracellular adenine nucleotides such as
 CC ATP and ADP. In pancreatic islets, may mediate some of the effects
 CC of extracellular ATP on insulin secretion.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; U22829; AAA91302.1; -.
 DR EMBL; AJ245636; CAB57317.1; -.
 DR HSSP; P34996; 1DDD.
 DR MGD; MGI:105049; P2ry1.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 52 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 53 74 1 (POTENTIAL).
 FT DOMAIN 75 87 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 88 109 2 (POTENTIAL).
 FT DOMAIN 110 126 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 127 147 3 (POTENTIAL).
 FT DOMAIN 148 166 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 167 188 4 (POTENTIAL).
 FT DOMAIN 189 218 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 219 238 5 (POTENTIAL).
 FT DOMAIN 239 265 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 266 285 6 (POTENTIAL).
 FT DOMAIN 286 303 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 304 328 7 (POTENTIAL).
 FT DOMAIN 329 373 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 124 202 BY SIMILARITY.
 FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 373 AA; 42212 MW; 944125E9F4560BB3 CRC64;

Query Match 28.8%; Score 475; DB 1; Length 373;
 Best Local Similarity 37.3%; Pred. No. 2.7e-24;
 Matches 107; Conservative 55; Mismatches 117; Indels 8; Gaps 7;

Qy 20 YYLSAFYAIEFIFGLLGNTVVFGYLFCKMKNWNSSNVYLFNLSISDFAFLCTLPLIKSY 79
 ||| | | : || | || : : || | : :||| :||| :||| :|||

Db 52 YYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFY 111

QY 80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILI 138

Db 112 FNKTDWIFGDAMCKLQRFIFHVNLVYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAIYV 171

QY 139 SLAVWALVTLEVLPLMTFFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197

Db 172 SVLVWLIVVVAISPILFYSGTGTRKNKTVTCYDTTSNDYLRYSYFIYSMCTTVAMFCIPL- 230

QY 198 VMCFFYYKMVVFLKRRSQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL 256

Db 231 VLILGCYGLIV--KALIYNDLDNSPLRRKSIYLVIIIVLTVFAVSYIPFHVMTMNLRLARL 288

QY 257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301

Db 289 DFQTPEMCDFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335

RESULT 4

P2YR_BOVIN

ID P2YR_BOVIN STANDARD; PRT; 373 AA.

AC P48042;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).

GN P2RY1.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Aortic endothelium;

RX MEDLINE=95352058; PubMed=7626079;

RA Henderson D.J., Elliot D.G., Smith G.M., Webb T.E., Dainty I.A.;

RT "Cloning and characterisation of a bovine P2Y receptor.;"

RL Biochem. Biophys. Res. Commun. 212:648-656(1995).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Corpus callosum;

RX MEDLINE=99064562; PubMed=9848096;

RA Deng G., Matute C., Kumar C.K., Fogarty D.J., Miledi R.;

RT "Cloning and expression of a P2y purinoceptor from the adult bovine corpus callosum.;"

RL Neurobiol. Dis. 5:259-270(1998).

CC -!- FUNCTION: Receptor for extracellular adenine nucleotides such as ATP and ADP.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

CC -----
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CC -----

DR EMBL; X87628; CAA60958.1; -.
DR EMBL; U34041; AAC78275.1; -.
DR PIR; JC4162; JC4162.
DR HSSP; P34996; 1DDD.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 52 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 53 74 1 (POTENTIAL).
FT DOMAIN 75 87 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 88 109 2 (POTENTIAL).
FT DOMAIN 110 126 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 127 147 3 (POTENTIAL).
FT DOMAIN 148 166 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 167 188 4 (POTENTIAL).
FT DOMAIN 189 218 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 219 238 5 (POTENTIAL).
FT DOMAIN 239 265 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 266 285 6 (POTENTIAL).
FT DOMAIN 286 303 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 328 7 (POTENTIAL).
FT DOMAIN 329 373 CYTOPLASMIC (POTENTIAL).
FT DISULFID 124 202 BY SIMILARITY.
FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 373 AA; 42287 MW; 9270A7175C0BDA76 CRC64;

Query Match 28.7%; Score 474; DB 1; Length 373;
Best Local Similarity 36.6%; Pred. No. 3.1e-24;
Matches 105; Conservative 58; Mismatches 116; Indels 8; Gaps 6;

Qy 20 YYLSAFYAIEFIFGLLGNTVVFGYLFCKMKNWNSSNVYLEFNLSISDEAFGLCTLPILIKSY 79
| | | | : | | | | : : : | | | : | : | : | : | : | | | |
Db 52 YYLPAVYIILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFY 111

Qy 80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISM DRYLLMKYPPFREFHFLQKKEFAILI 138
| : | : | | : : | | | | | | | | | | : | : | : | : |
Db 112 FNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKNVYI 171

Qy 139 SLAVWALVTLEVLPLMTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
| : | | : | : : | : | : : | : | | | | | : | : | : | : |
Db 172 SVLVWLIVVVGISPILFYSGTGIRKNKTITCYDTTSDEYLRYSYFIYSMCTTVAMFCVPLV 231

Qy 198 VMCFYYKMOVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIRASRL 256
: : | : | | : : | | | | : : : : : : : : : : : : : :
Db 232 LILGCGYLIVRALIYKDLDNS---PLRRKSIYLVIIIVLTVFAVSYIPFHVMTMNLRLARL 288

Qy 257 D-SWPQGCT-QKAISYITLRLPLAFLNSAINPIFYFLMGDHYREML 301

Db 289 DFQTPMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335

RESULT 5

P2YR_HUMAN

ID P2YR_HUMAN STANDARD; PRT; 373 AA.
AC P47900;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
GN P2RY1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=96257237; PubMed=8666290;
RA Leon C., Vial C., Cazenave J.-P., Gachet C.;
RT "Cloning and sequencing of a human cDNA encoding endothelial P2Y1
RT purinoceptor.";
RL Gene 171:295-297(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96158962; PubMed=8579591;
RA Ayyanathan K., Tania W., Harbansjit S., Raghbir A.S., Barnard E.A.,
RA Kunapuli S.P.;
RT "Cloning and chromosomal localization of the human P2Y1
RT purinoceptor.";
RL Biochem. Biophys. Res. Commun. 218:783-788(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96205320; PubMed=8630005;
RA Janssens R., Communi D., Pirotton S., Samson M., Parmentier M.,
RA Boeynaems J.M.;
RT "Cloning and tissue distribution of the human P2Y1 receptor.";
RL Biochem. Biophys. Res. Commun. 221:588-593(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Leon C., Vial C., Weber J., Cazenave J.-P., Gacher C.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN [6]
RP SEQUENCE OF 95-373 FROM N.A., FUNCTION, AND INHIBITION STUDIES.
RC TISSUE=Platelet;
RX MEDLINE=98113162; PubMed=9442040;
RA Jin J., Daniel J.L., Kunapuli S.P.;

RT "Molecular basis for ADP-induced platelet activation. II. The P2Y1
RT receptor mediates ADP-induced intracellular calcium mobilization and
RT shape change in platelets.";
RL J. Biol. Chem. 273:2030-2034(1998).
CC -!- FUNCTION: Receptor for extracellular adenine nucleotides such as
CC ATP and ADP. In platelets binding to ADP leads to mobilization of
CC intracellular calcium ions via activation of phospholipase C, a
CC change in platelet shape, and probably to platelet aggregation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- INDUCTION: Repressed by the P2Y1 receptor-specific antagonists
CC A3P5PS, A3P5P and A2P5P. These inhibit calcium ion mobilization
CC and shape change in platelets.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
DR EMBL; Z49205; CAA89066.1; -.
DR EMBL; U42030; AAA97873.1; -.
DR EMBL; U42029; AAA97872.1; -.
DR EMBL; S81950; AAB47091.1; -.
DR EMBL; AJ006945; CAA07339.1; -.
DR EMBL; AY136752; AAN01278.1; -.
DR EMBL; AF018284; AAB94556.1; -.
DR PIR; JC4737; JC4737.
DR HSSP; P34996; 1DDD.
DR Genew; HGNC:8539; P2RY1.
DR MIM; 601167; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . . ; TAS.
DR GO; GO:0007200; P:G-protein signaling, coupled to IP3 second . . . ; TAS.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Platelet;
KW Blood coagulation.
FT DOMAIN 1 52 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 53 74 1 (POTENTIAL).
FT DOMAIN 75 87 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 88 109 2 (POTENTIAL).
FT DOMAIN 110 126 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 127 147 3 (POTENTIAL).
FT DOMAIN 148 166 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 167 188 4 (POTENTIAL).
FT DOMAIN 189 218 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 219 238 5 (POTENTIAL).
FT DOMAIN 239 265 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 266 285 6 (POTENTIAL).
FT DOMAIN 286 303 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 304 328 7 (POTENTIAL).
 FT DOMAIN 329 373 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 124 202 BY SIMILARITY.
 FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 138 138 MISSING (IN REF. 1).
 SQ SEQUENCE 373 AA; 42071 MW; 4DC7C668B4145392 CRC64;

Query Match 28.7%; Score 474; DB 1; Length 373;
 Best Local Similarity 37.3%; Pred. No. 3.1e-24;
 Matches 107; Conservative 55; Mismatches 117; Indels 8; Gaps 6;

QY 20 YYLSAFYAIEFIFGLLGNTVVFGYLFCKMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79
 ||| | | : || | ||| :: ::| || |: :||:||||::|| :: ||| || |
 Db 52 YYLPAVYILVFIIGFLGNSVAIWMFVHFHMKPWSGISVYMFNLALADFLYVLTLPALIFY 111
 QY 80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFSMDRYLLMKYPFREHFLQKKEFAILI 138
 | :|| :| |:: | ||| ||||| || || : || : ||: || |
 Db 112 FNKTDWIFGDAMCKLQRFIFHVNLGYSILFLTCSAHRYSGVVYPLKSLGRLKKKNAICI 171
 QY 139 SLAVWALVTLEVLPLMTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
 |: || :| : : |:| : : | | : | | | ||:| |: | :||
 Db 172 SVLVWLIVVVAISPILFYSGTGVKKNKTITCYDTTSDEYLRSYFIYSMCTTVAMFCVPLV 231
 QY 198 VMCFYYKMOVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL 256
 :: | :| | : : || | ||:: : :||: : |:|:|: : : :||
 Db 232 LILGCYGLIVRALIYKDLNS---PLRRKSIYLVIIVLTVFAVSYPFHVMTKTMNLRARL 288
 QY 257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
 | | | : : | :|| || ||| ::|| ||| || :| |
 Db 289 DFQTPAMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335

RESULT 6

P2YR_CHICK

ID P2YR_CHICK STANDARD; PRT; 362 AA.
 AC P34996;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
 GN P2RY1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93285340; PubMed=8508924;
 RA Webb T.E., Simon J., Krishek B.J., Bateson A.N., Smart T.G.,
 RA King B.F., Burnstock G., Barnard E.A.;
 RT "Cloning and functional expression of a brain G-protein-coupled ATP
 RT receptor.";

RL FEBS Lett. 324:219-225(1993).
 RN [2]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=97026278; PubMed=8872457;
 RA van Rhee A.M., Fischer B., van Galen P.J.M., Jacobson K.A.;
 RT "Modelling the P2Y purinoceptor using rhodopsin as template";
 RL Drug Des. Discov. 13:133-140(1995).
 CC -!- FUNCTION: Receptor for extracellular adenine nucleotides such as
 CC ATP and ADP. Seems to mediate its action via a pertussis toxin
 CC insensitive G-protein, probably belonging to the Gq family that
 CC activate a phosphatidylinositol-calcium second messenger system.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Brain, spinal cord, gastrointestinal tract,
 CC spleen and leg muscle. Is not detected in the heart, liver,
 CC stomach, lung and kidney.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; X73268; CAA51716.1; -.
 DR PIR; S33733; S33733.
 DR PDB; 1DDD; 11-JUL-96.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; 3D-structure.
 FT DOMAIN 1 41 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 42 63 1 (POTENTIAL).
 FT DOMAIN 64 76 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 77 98 2 (POTENTIAL).
 FT DOMAIN 99 115 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 116 136 3 (POTENTIAL).
 FT DOMAIN 137 155 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 156 177 4 (POTENTIAL).
 FT DOMAIN 178 207 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 208 227 5 (POTENTIAL).
 FT DOMAIN 228 254 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 255 274 6 (POTENTIAL).
 FT DOMAIN 275 292 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 293 317 7 (POTENTIAL).
 FT DOMAIN 318 362 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 113 191 BY SIMILARITY.
 FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT HELIX 42 69
 FT HELIX 77 102
 FT HELIX 115 137

FT HELIX 154 178
 FT HELIX 205 231
 FT HELIX 250 275
 FT HELIX 290 305
 FT TURN 306 307
 FT HELIX 308 320
 SQ SEQUENCE 362 AA; 41194 MW; A806C88FB9514761 CRC64;

Query Match 28.6%; Score 472.5; DB 1; Length 362;
 Best Local Similarity 35.9%; Pred. No. 3.8e-24;
 Matches 110; Conservative 58; Mismatches 121; Indels 17; Gaps 8;

QY 10 WLA---TEAILNK-----YYLSAFYAIEFIFGLLGNTVVFGYLFCKMKNWNSSNVYLEFN 60
 | | | : | | | | : | | | | : : | : | : | : |
 Db 22 WAAGNATTKCSLTKTGFQFYLLPTVYILVFITGFLGNSVAIWMFVHMRPWSGISVYMFN 81
 QY 61 LSISDFAFLCTLPLILIKSYANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLL 119
 | : : | : : | | | | | : | : | | | | | | : | : |
 Db 82 LALADFLYVLTLPALIFYFENKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISVHRYTG 141
 QY 120 MKYPPFHEHFLQKKEFAILISLAWALVTLEVLPLMTFINS-VPKEEGSNCIDYASSGNPE 178
 : : | : | : | : | | : | : | : | : | : | : | :
 Db 142 VVHPLKSLGRLKKKNNAVYVSSLVWALVAVIAPILFYSGTGVRNKTITCYDTTADAYLR 201
 QY 179 HNLIYSLCLTLLGFLIPLSVMCFYYKVVFLKRRSQQQATALPL-DKPQRLVVLAVVIF 237
 : | : | | : | | | : | : | : | : | : | : | : | :
 Db 202 SYFVYSMCTTVFMFCIPFIVILGCYGLIVKALIYKDLDNS---PLRRKSIYLVIIIVLTVF 258
 QY 238 SILFTPYHIMRNLRIASRLD-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGD 295
 : : : | : | : | : : | | | : : | : | | | : | | | |
 Db 259 AVSYLPFHVMKTLNLRARLDFQTPQMCAFNKQVYATYQVTRGLASLNSCVDPIYFLAGD 318
 QY 296 HYREML 301
 : | |
 Db 319 TFRRL 324

RESULT 7

P2YR_MELGA

ID P2YR_MELGA STANDARD; PRT; 362 AA.
 AC P49652;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor) (6H1
 DE orphan receptor).
 GN P2RY1.
 OS Meleagris gallopavo (Common turkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
 OX NCBI_TaxID=9103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=94335907; PubMed=8058061;
 RA Filtz T.M., Li Q., Boyer J.L., Nicholas R.A., Harden T.K.;
 RT "Expression of a cloned P2Y purinergic receptor that couples to

RT phospholipase C.";
 RL Mol. Pharmacol. 46:8-14(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97382456; PubMed=9240460;
 RA Li Q., Schachter J.B., Harden T.K., Nicholas R.A.;
 RT "The 6H1 orphan receptor, claimed to be the p2y5 receptor, does not
 RT mediate nucleotide-promoted second messenger responses.";
 RL Biochem. Biophys. Res. Commun. 236:455-460(1997).
 CC -!- FUNCTION: Receptor for extracellular adenine nucleotides such as
 CC ATP and ADP. Seems to mediate its action via a pertussis toxin
 CC insensitive G-protein, probably belonging to the Gq family that
 CC activate a phosphatidylinositol-calcium second messenger system.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Mainly found in blood, brain, and lung. To a
 CC lesser extent in stomach, gut and skeletal muscle.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; U09842; AAA18784.1; -.
 DR EMBL; AF012103; AAB65428.1; -.
 DR HSSP; P34996; 1DDD.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 41 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 42 63 1 (POTENTIAL).
 FT DOMAIN 64 76 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 77 98 2 (POTENTIAL).
 FT DOMAIN 99 115 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 116 136 3 (POTENTIAL).
 FT DOMAIN 137 155 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 156 177 4 (POTENTIAL).
 FT DOMAIN 178 207 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 208 227 5 (POTENTIAL).
 FT DOMAIN 228 254 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 255 274 6 (POTENTIAL).
 FT DOMAIN 275 292 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 293 317 7 (POTENTIAL).
 FT DOMAIN 318 362 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 113 191 BY SIMILARITY.
 FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 362 AA; 41180 MW; 3E128AB9EB64349C CRC64;

Query Match 28.6%; Score 472.5; DB 1; Length 362;
 Best Local Similarity 35.9%; Pred. No. 3.8e-24;
 Matches 110; Conservative 58; Mismatches 121; Indels 17; Gaps 8;

Qy 10 WLA----TEAILNK-----YYLSAFYAIEFIFGLLGNVTVVFGYLFCKMKNWNSSNVYLFN 60
 | | | : | | | | | : | | | | | : : | | : | : | : | : |
 Db 22 WAAGNASTKCSLTKTGFQFYLLPTVYILVFITGFLGNSVAIWMFVFHMRPWSGISVYMEN 81
 Qy 61 LSISDFAFLCTLPLILIKSYANDKG-TYGDVLCISNRYVLHTNLTYTSILFLTFISMTRYLL 119
 | : : | | : : | | | | | | : | | : | | | | | | | : | |
 Db 82 LALADFLYVLTLPALIFYFENKTDWIFGDMCKLQRFIFHVNLYGSILFLTCISVHRYTG 141
 Qy 120 MKYPFREFHFLQKKEFAILISLAWALVTLEVLPMLTFINS-VPKEEGSNCIDYASSGNPE 178
 : : | : | : | : | : | | | | : | : | : : | : : | : :
 Db 142 VVHPLKSLGRLKKKNAVYVSSLVWALVAVIAPILFYSGTGVRNRKTITCYDTTADDEYLR 201
 Qy 179 HNLIYSLCLTLLGFLIPLSVMCFYYKMMVFLKRRSQQATALPL-DKPQRLVVLAVVIF 237
 : | : | | : | | | : | : | : : | | | | : : : : |
 Db 202 SYFVYSMCTTVFMFCIPFIVILGCYGLIVKALIYKDLDNS---PLRRKSIYLVIIIVLTVF 258
 Qy 238 SILFTPYHIMRNLRIRASRLD-SWPQGCT-QKAISYITLRLPLAFNLNSAINPIFYFLMGD 295
 : : : | : | : | : : | | | | : : | : | | | | : : | | | |
 Db 259 AVSYLPFHVMTLNLRLARLDFQTPQMCAFNQKVYATYQVTRGLASLNSCVDPIYFLAGD 318
 Qy 296 HYREML 301
 : | |
 Db 319 TFRRL 324

RESULT 8

GP80_HUMAN

ID GP80_HUMAN STANDARD; PRT; 337 AA.
 AC Q96P68; Q86TL1;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Probable G protein-coupled receptor GPR80 (P2Y-like nucleotide
 DE receptor) (P2Y-like GPCR).
 GN GPR80 OR GPR99.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21458557; PubMed=11574155;
 RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,
 RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
 RT "Discovery and mapping of ten novel G protein-coupled receptor
 RT genes.";
 RL Gene 275:83-91(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX PubMed=12098360;
 RA Wittenberger T., Hellebrand S., Munck A., Kreienkamp H.-J.,
 RA Schaller H.C., Hampe W.;

RT "GPR99, a new G protein-coupled receptor belonging to a new subgroup
 RT of nucleotide receptors.";
 RL BMC Genomics 3:17-17(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22040266; PubMed=12044878;
 RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
 RT "Identification of G protein-coupled receptor genes from the human
 RT genome sequence.";
 RL FEBS Lett. 520:97-101(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 RT receptor genes.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thyroid;
 RA Bruess M., Bonisch H., von Kugelgen I.;
 RT "Molecular cloning and functional characterization of a new human P2Y
 RT receptor.";
 RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Orphan receptor.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Detected in kidney and, to a lower extend, in
 CC placenta. Not detected in brain tissues including the frontal
 CC cortex, caudate putamen, thalamus, hypothalamus, hippocampus or
 CC pons.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC -----
 DR EMBL; AF411109; AAL26480.1; -.
 DR EMBL; AF370886; AAM76912.1; -.
 DR EMBL; AB083598; BAB89311.1; -.
 DR EMBL; AB065877; BAC06095.1; -.
 DR EMBL; AJ305372; CAC83857.1; -.
 DR Genew; HGNC:4531; GPR80.
 DR MIM; 606922; -.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 35 55 1 (POTENTIAL).
 FT DOMAIN 56 69 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 70 90 2 (POTENTIAL).

FT	DOMAIN	91	116	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	117	137	3 (POTENTIAL).
FT	DOMAIN	138	151	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	152	172	4 (POTENTIAL).
FT	DOMAIN	173	201	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	202	222	5 (POTENTIAL).
FT	DOMAIN	223	242	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	243	263	6 (POTENTIAL).
FT	DOMAIN	264	284	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	285	305	7 (POTENTIAL).
FT	DOMAIN	306	337	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	106	183	BY SIMILARITY.
FT	CARBOHYD	10	10	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	23	23	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	176	176	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	179	179	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	14	14	F -> L (IN REF. 5).
FT	CONFLICT	236	236	K -> R (IN REF. 5).
SQ	SEQUENCE	337 AA; 38251 MW; 6814EA0044756CE6 CRC64;		

Query Match 25.8%; Score 426; DB 1; Length 337;
 Best Local Similarity 34.4%; Pred. No. 3.8e-21;
 Matches 101; Conservative 57; Mismatches 126; Indels 10; Gaps 6;

QY	17	LNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCKMKNWNSSNVYLFNLSISDFAFLCTLPILI	76
		: : : : : : : : : :	
Db	31	LKMHYLPVIYGIIFLVGFPGNAVVISYIFKMRPWKSSTIIMLNLA CTDLLYLTSLPFLI	90
QY	77	KSYAN-DKGTYG DVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFA	135
		: : : : : : : : : :	
Db	91	HYASGENWIFGDFMCKFIRSFHFNLYSSILFLTCFSIFRYCVIIHPMSCFSIHKTRCA	150
QY	136	ILISLAVWALVTLEVLPM LTFINSVPKEEGSNCIDYASSGNPEHNLI--YSLCLTLLGFL	193
		: : : : : : : :	
Db	151	VVACAVVWIISLVAVIPMTFLTITSTNRTRNSACLDLTSS--DELNTIKWYNLILTATTCF	208
QY	194	IPLSVMCFFYYKMV VFLKRRSQQQATALPLDKPQRLVVLAVVIFSI LFTPYHIMRNLR	253
		: : : : : : : : : : : : : :	
Db	209	LPLVIVTLCYTTIIHTLTHGLQTD SCL--KQKARRLTILLLLAFYVCFLPFHILRVIRIE	266
QY	254	SRLD SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFR	306
		: : : : : : : : : : : :	
Db	267	SRLLS--ISCSIENQIHEAYIVSRPLAALNTFGNLLLYVVVSDNFQQAVCSTVR	318

RESULT 9

P2Y8_XENLA

ID P2Y8_XENLA STANDARD; PRT; 537 AA.

AC P79928;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE P2Y purinoceptor 8 (P2Y8).

GN P2RY8.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Neural plate;
 RX MEDLINE=97284734; PubMed=9139711;
 RA Bogdanov Y.D., Dale L., King B.F., Whittock N., Burnstock G.;
 RT "Early expression of a novel nucleotide receptor in the neural plate
 RT of Xenopus embryos.";
 RL J. Biol. Chem. 272:12583-12590(1997).
 CC -!- FUNCTION: Receptor for extracellular ATP, UTP, CTP, GTP and ITP.
 CC The activity of this receptor is mediated by G proteins which
 CC activate a phosphatidylinositol-calcium second messenger system.
 CC May play a key role in the early development of neural tissue.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; X99953; CAA68213.1; -.
 DR HSSP; P34996; 1DDD.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 49 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 50 70 1 (POTENTIAL).
 FT DOMAIN 71 79 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 80 100 2 (POTENTIAL).
 FT DOMAIN 101 118 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 119 139 3 (POTENTIAL).
 FT DOMAIN 140 161 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 162 182 4 (POTENTIAL).
 FT DOMAIN 183 210 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 211 231 5 (POTENTIAL).
 FT DOMAIN 232 254 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 255 275 6 (POTENTIAL).
 FT DOMAIN 276 292 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 293 316 7 (POTENTIAL).
 FT DOMAIN 317 537 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 116 193 BY SIMILARITY.
 FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 537 AA; 62024 MW; B2CF24812F3C19F2 CRC64;

Query Match 23.4%; Score 386.5; DB 1; Length 537;
 Best Local Similarity 35.3%; Pred. No. 2.1e-18;
 Matches 104; Conservative 51; Mismatches 125; Indels 15; Gaps 7;

QY 22 LSAFYAIEFIFGLLGNTVWFGYLEFCMKNWNSSNVYLFNLSISDFAFLCTLPLILIKSYAN 81
 | : | : | : | : : : : | : | : | : | : | : : | : | : | :
 Db 46 LPVSYSAVFMVGLPLNIAAMWIFIAMRPWNPTTVYMFNLALSDTLVLSLPTLVYVYA- 104
 QY 82 DKGT--YGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILIS 139
 | : | : | : | : : | : | : | : | : | : | : | : | : | : | :
 Db 105 DKNWPFGEVLCKLVRFLFYANLYSSILFLTCISVHRYRGVCHPITSLRRMNAKHAYVIC 164
 QY 140 LAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLSVM 199
 | : | : | : | : | : | : | : | : | : | : | : | : | : | :
 Db 165 ALVWLSVTLCIVPNLIFVTVSPKVKNITICHDTTRPEDFARYVEYSTAIMCLLFGIPCLII 224
 QY 200 CFFYYKMVFLKRR--SQQQATALPLDKPQ--RLVVLAVVIFSILFTPYHIMRNLRISAR 255
 | : | : | : | : | : | : | : | : | : | : | : | : | : | :
 Db 225 AGCYGLMTRELMKPIVSGNQQT-LPSYKKRSIKTIIFVMIAFAICFMPFHITRTLYYYAR 283
 QY 256 LDSWPQGCTQKAIKSI---YTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQ 307
 | : | : | : | : | : | : | : | : | : | : | : | : | : | :
 Db 284 L----LGIKCYALNVINVTYKVTRPLASANS CIDPILYFLANDRYRRRLIRTVRR 334

RESULT 10

P2Y3_CHICK

ID P2Y3_CHICK STANDARD; PRT; 328 AA.
 AC Q98907;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE P2Y purinoceptor 3 (P2Y3) (Nucleoside diphosphate receptor).
 GN P2RY3.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96319774; PubMed=8700132;
 RA Webb T.E., Henderson D., King B.F., Wang S., Simon J.,
 RA Bateson A.N., Burnstock G., Barnard E.A.;
 RT "A novel G protein-coupled P2 purinoceptor (P2Y3) activated
 RT preferentially by nucleoside diphosphates.";
 RL Mol. Pharmacol. 50:258-265(1996).
 CC -!- FUNCTION: Receptor for extracellular ADP > UTP > ATP = UDP. The
 CC activity of this receptor is mediated by G proteins which activate
 CC a phosphatidylinositol-calcium second messenger system.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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CC -----
 DR EMBL; X98283; CAA66930.1; -.
 DR HSSP; P34996; 1DDD.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 22 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 23 43 1 (POTENTIAL).
 FT DOMAIN 44 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 58 78 2 (POTENTIAL).
 FT DOMAIN 79 96 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 97 117 3 (POTENTIAL).
 FT DOMAIN 118 139 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 140 160 4 (POTENTIAL).
 FT DOMAIN 161 189 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 190 210 5 (POTENTIAL).
 FT DOMAIN 211 231 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 232 252 6 (POTENTIAL).
 FT DOMAIN 253 275 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 276 298 7 (POTENTIAL).
 FT DOMAIN 299 323 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 94 172 BY SIMILARITY.
 SQ SEQUENCE 328 AA; 37586 MW; 7A3BF1C91F54FAAB CRC64;

Query Match 23.0%; Score 379.5; DB 1; Length 328;
 Best Local Similarity 29.6%; Pred. No. 3.9e-18;
 Matches 88; Conservative 63; Mismatches 135; Indels 11; Gaps 4;

QY 22 LSAFYAIEFIFGLLGNVTVVFGYLCMKNNWSSNVYLENLSISDFAFLCTLPILIKSYA- 80
 | : : | : | : | : : : : | : : : : | : : : : | : :
 Db 24 LPLVYSVVFLGLPLNAVIGQIWLARKALTRTTIYMLNLAMADLLYVCSLPLLIYNYTQ 83
 QY 81 NDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFRE-HFLQKKEFAILIS 139
 | : : | : | : : : : | : : : : | : : : : | : : : : | : :
 Db 84 KDYWPFGDFTCKFVRFQFYTNLHGSILFLTCISVQRYMGICHPLASWHKKKGKKLTWLVC 143
 QY 140 LAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLSVM 199
 | : : | : | : : : : | : : : : | : : : : | : : : : | : :
 Db 144 AAVWFIVIAQCLPTFVFFASTGTQRNRTVCYDLSPDRSTSYFPYGITLTITGFLLPFAAI 203
 QY 200 CFFYYKMVFLKRRSQQAATAL--PLDKPQRLVVLAVVIFSILFTPYHIMRNLRIASRLD 257
 | : : | : : : : | : : : : | : : : : | : : : : | : : : : | : :
 Db 204 LACYCSMARILCQKDELIGLAVHKKKDKAVRMIIIVVIVFSISFFPFHLTKTIYLVIRSS 263
 QY 258 SWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE-----MLISKFRQ 307
 : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : :
 Db 264 ASLPCPTLQAFIAIAYKCTRPFASMNSVLDPIIFYFTQKRFRESTRYLLDKMSSKWRQ 320

RESULT 11
 P2Y2_RAT
 ID P2Y2_RAT STANDARD; PRT; 374 AA.
 AC P41232;

DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE P2Y purinoceptor 2 (P2Y2) (P2U purinoceptor 1) (P2U1) (ATP receptor)
 DE (Purinergic receptor).
 GN P2RY2 OR P2RU1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95110548; PubMed=7811468;
 RA Rice W.R., Burton F.M., Fiedelvey D.T.;
 RT "Cloning and expression of the alveolar type II cell P2u-purinergic
 RT receptor.";
 RL Am. J. Respir. Cell Mol. Biol. 12:27-32(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Pituitary;
 RA Chen Z.P., Krull N., Xu S., Levy A., Lightman S.L.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar;
 RX MEDLINE=98099857; PubMed=9437211;
 RA Seye C.I., Gadeau A.P., Daret D., Dupuch F., Alzieu P., Capron L.,
 RA Desgranges C.;
 RT "Overexpression of P2Y2 purinoceptor in intimal lesions of the rat
 RT aorta.";
 RL Arterioscler. Thromb. Vasc. Biol. 17:3602-3610(1997).
 CC -!- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that
 CC activate a phosphatidylinositol-calcium second messenger system.
 CC The affinity range is UTP = ATP > ATP-gamma-S >> 2-methylthio-ATP
 CC = ADP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; U09402; AAA61565.1; -.
 DR EMBL; L46865; AAB02099.1; -.
 DR EMBL; U56839; AAC00048.1; -.
 DR HSSP; P34996; 1DDD.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	33	59	1 (POTENTIAL).
FT	DOMAIN	60	70	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	71	93	2 (POTENTIAL).
FT	DOMAIN	94	110	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	111	129	3 (POTENTIAL).
FT	DOMAIN	130	152	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	153	172	4 (POTENTIAL).
FT	DOMAIN	173	194	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	195	220	5 (POTENTIAL).
FT	DOMAIN	221	245	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	246	268	6 (POTENTIAL).
FT	DOMAIN	269	286	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	287	308	7 (POTENTIAL).
FT	DOMAIN	309	374	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	9	9	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	13	13	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	106	183	BY SIMILARITY.
FT	CONFLICT	132	132	C -> S (IN REF. 1).
FT	CONFLICT	143	143	S -> R (IN REF. 1).
FT	CONFLICT	166	166	A -> T (IN REF. 1).
FT	CONFLICT	188	188	A -> D (IN REF. 1).
SQ	SEQUENCE	374 AA;	42137 MW;	2DA6853AA20A1AF3 CRC64;

Query Match 22.7%; Score 374; DB 1; Length 374;
 Best Local Similarity 33.8%; Pred. No. 9.8e-18;
 Matches 96; Conservative 50; Mismatches 124; Indels 14; Gaps 7;

Qy	19	KY-YLSAFYAIEFIFGLLGNVTVVFGYLFCKMKNWNSSNVYLFNLSISDFAFLCTLPILIK	77
		: : :: : : : : : : : :	
Db	32	KYVLLPVSYGVVCVLGLCLNVVALYIFLCRLKTWNASTTYMFHLAVSDSLYAASLPLLVY	91
Qy	78	SYA-NDKGTYGDLVCISNRYVLHTNLYTSILFLTIFISMDRYLLMKYPFREFHFLQKKEFAI	136
		: :: : : : :	
Db	92	YYAQGDHWPFSTVLCKLVREFLYTNLYCSILFLTCISVHRCGLVLRPLHSLSWGHARYAR	151
Qy	137	LISLAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLGLFLIPL	196
		:: : : : : :: : : :	
Db	152	RVAAVVWVLVLACQAPVLYFVTTSVRGTRITCHDTSARELFSHFVAYSSVMLGLLEAVPF	211
Qy	197	SVMCFFYYKMVFLKRRSQQQA---TALPLDKPQ--RLVVLAUVIFSILFTPYHIMRNLR	251
		:: : : : : : : : :	
Db	212	SIILVCY----VLMARLLKPAYGTTGLPRAKRKSVRTIALVLAVFALCFLPFHVTRTLY	267
Qy	252	IASRLDSWPQGC-TQKAIKSIYTLTRPLAFLNSAINPIFYFLMG	294
		: : :: :	
Db	268	YSFR--SLDLSCHTLNAINMAYKITRPLASANSCLDPVLYFLAG	309

RESULT 12

P2Y2_MOUSE

ID P2Y2_MOUSE STANDARD; PRT; 373 AA.
 AC P35383; O09031; Q9CPZ4;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE P2Y purinoceptor 2 (P2Y2) (P2U purinoceptor 1) (P2U1) (ATP receptor)
 DE (Purinergic receptor).

GN P2RY2 OR P2RU1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93281707; PubMed=7685114;
 RA Lustig K.D., Shiau A.K., Brake A.J., Julius D.;
 RT "Expression cloning of an ATP receptor from mouse neuroblastoma
 RT cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:5113-5117(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96316177; PubMed=8739319;
 RA Enomoto K., Furuya K., Moore R.C., Yamagishi S., Oka T., Maeno T.;
 RT "Expression cloning and signal transduction pathway of P2U receptor
 RT in mammary tumor cells.";
 RL Biol. Signals 5:9-21(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head, and Liver;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast tumor;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP MUTAGENESIS OF LYS-107; ARG-110; HIS-262; ARG-265; LYS-289 AND
 RP ARG-292.
 RX MEDLINE=95181393; PubMed=7876172;
 RA Erb L., Garrad R.C., Wang Y., Quinn T., Turner J.T., Weisman G.A.;
 RT "Site-directed mutagenesis of P2U purinoceptors. Positively charged
 RT amino acids in transmembrane helices 6 and 7 affect agonist potency
 RT and specificity.";
 RL J. Biol. Chem. 270:4185-4188(1995).
 CC -!- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that
 CC activate a phosphatidylinositol-calcium second messenger system.
 CC The affinity range is UTP = ATP > ATP-gamma-S >> 2-methylthio-ATP
 CC = ADP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Spleen, testis, kidney, liver, lung, heart and
 CC brain.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; L14751; AAA39871.1; -.
 DR EMBL; S83099; AAB50735.1; -.
 DR EMBL; AK005013; BAB23746.1; -.
 DR EMBL; AK017378; BAB30719.1; -.
 DR EMBL; BC006613; AAH06613.1; -.
 DR PIR; A47556; A47556.
 DR HSSP; P34996; 1DDD.
 DR MGD; MGI:105107; P2ry2.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 33 59 1 (POTENTIAL).
 FT DOMAIN 60 70 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 71 93 2 (POTENTIAL).
 FT DOMAIN 94 110 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 111 129 3 (POTENTIAL).
 FT DOMAIN 130 152 CYTOPLASMIC (POTENTIAL).

FT	TRANSMEM	153	172	4 (POTENTIAL).
FT	DOMAIN	173	194	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	195	220	5 (POTENTIAL).
FT	DOMAIN	221	246	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	247	269	6 (POTENTIAL).
FT	DOMAIN	270	287	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	288	309	7 (POTENTIAL).
FT	DOMAIN	310	373	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	9	9	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	13	13	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	106	183	BY SIMILARITY.
FT	MUTAGEN	107	107	K->I: NO EFFECT ON RECEPTOR ACTIVATION.
FT	MUTAGEN	110	110	R->L: NO EFFECT ON RECEPTOR ACTIVATION.
FT	MUTAGEN	262	262	H->L: DECREASE IN RECEPTOR ACTIVATION.
FT	MUTAGEN	265	265	R->L: DECREASE IN RECEPTOR ACTIVATION.
FT	MUTAGEN	289	289	K->I: NO EFFECT ON RECEPTOR ACTIVATION.
FT	MUTAGEN	292	292	R->L: DECREASE IN RECEPTOR ACTIVATION.
FT	CONFLICT	17	17	E -> D (IN REF. 2).
FT	CONFLICT	120	120	S -> R (IN REF. 2).
FT	CONFLICT	125	125	T -> N (IN REF. 2).
FT	CONFLICT	196	196	V -> M (IN REF. 2).
FT	CONFLICT	263	263	V -> L (IN REF. 3).
FT	CONFLICT	355	355	D -> N (IN REF. 2).
FT	CONFLICT	369	371	KDI -> PYV (IN REF. 2).
SQ	SEQUENCE	373 AA;	42174 MW;	590BBE502E41B3AE CRC64;

Query Match 22.6%; Score 373.5; DB 1; Length 373;
 Best Local Similarity 33.5%; Pred. No. 1.1e-17;
 Matches 94; Conservative 50; Mismatches 130; Indels 7; Gaps 5;

QY	19	KY-YLSAFYAIEFIFGLLGNVTVVFGYLFCKMKNWNSSNVYLFNLSISDFAFLCTLPILIK	77
Db	32	KYVLLPVSYGVCVLGLCLNVVALYIFLCRLKTWNASTTYMFHLAVSDSLYAASLPLLVY	91
QY	78	SYA-NDKGTYGDLVCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAI	136
Db	92	YYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRCLGVLRLPLHSLRWGRARYAR	151
QY	137	LISLAVWALVTLEVLPLMTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPL	196
Db	152	RVAADVWVLVLACQAPVLYFVTTSVRGTRITCHDTSARELFSHFVAYSSVMLGLLFAVPF	211
QY	197	SVMCFFYYKMVFLKRRSQQQATALPLDKPQ--RLVVLAUVIFSILFTPYHIMRNLRIS	254
Db	212	SVILVCYVLMARRLLKPAYGTTGGLPRAKRKSVRTIALVLAVFALCFLPFHVTRTLYYSF	271
QY	255	RLDSWPQGC-TQKAIKSIYTLTRPLAFLNSAINPIFYFLMG	294
Db	272	R--SLDLSCHTLNAINMAYKITRPLASANSCLDPVLYFLAG	310

RESULT 13

P2Y3_MELGA

ID P2Y3_MELGA STANDARD; PRT; 328 AA.

AC O93361;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE P2Y purinoceptor 3 (P2Y3) (Nucleoside diphosphate receptor).
 GN P2RY3.
 OS Meleagris gallopavo (Common turkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
 OX NCBI_TaxID=9103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98401046; PubMed=9730913;
 RA Li Q., Olesky M., Palmer R.K., Harden T.K., Nicholas R.A.;
 RT "Evidence that the p2y3 receptor is the avian homologue of the
 RT mammalian P2Y6 receptor."
 RL Mol. Pharmacol. 54:541-546(1998).
 CC -!- FUNCTION: RECEPTOR FOR EXTRACELLULAR UDP > ADP = UTP. THE ACTIVITY
 CC OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE A
 CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; AF069555; AAC23863.1; -.
 DR HSSP; P34996; 1DDD.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 22 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 23 43 1 (POTENTIAL).
 FT DOMAIN 44 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 58 78 2 (POTENTIAL).
 FT DOMAIN 79 96 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 97 117 3 (POTENTIAL).
 FT DOMAIN 118 139 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 140 160 4 (POTENTIAL).
 FT DOMAIN 161 189 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 190 210 5 (POTENTIAL).
 FT DOMAIN 211 231 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 232 252 6 (POTENTIAL).
 FT DOMAIN 253 275 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 276 298 7 (POTENTIAL).
 FT DOMAIN 299 323 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 94 172 BY SIMILARITY.
 SQ SEQUENCE 328 AA; 37594 MW; B74D49B99C7164A5 CRC64;

Query Match 22.5%; Score 371.5; DB 1; Length 328;
 Best Local Similarity 29.4%; Pred. No. 1.3e-17;

Matches 87; Conservative 61; Mismatches 137; Indels 11; Gaps 4;

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Qy      22 LSAFYAIEFIFGLLGNVTVVFYGLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSYA- 80
      |  |::|:| | | | : | : :|:|:| | :|:|:|:| | :|
Db      24 LPLVYSVVFLGLPLNAVVGQIWLARKALTRTTIYMLNLATADLLYVCSLPLLIYNYTQ 83

Qy      81 NDKGTYGDVLCISNRYVLHTNLTYTSILFLTIFISMDRYLLMKYPFRE-HFLQKKEFAILIS 139
      |  :|| | | : :||:| ||||| ||: ||: : :| | : | : | :
Db      84 KDYWPFGDFTCKFVRFQFYTNLHGSILFLTICISVQRYMGICHPLASWHKKKGKKLTWLVC 143

Qy     140 LAVWALVTLEVLPMLTFINSVPKKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLSVM 199
      ||| :| : || | :: : : | | : | : ||:| ||:| : :
Db     144 AAVWFIVIAQCLPTFVFASTGTQRNRTVCYDLSPDRSASYFPYGITLTITGFLLPFAAI 203

Qy     200 CFFYYKMVVFLKRRSQQQATAL--PLDKPQRLVVLAVVIFSILFTPYHIMRNLIASRLD 257
      | | | : : : | : || :|:|:| :|:|:| : : : |
Db     204 LACYCSMARILCQKDELIGLAVHKKKDKAVRMIIIVVIVFSISFFPFHLTKTIYLVIRSS 263

Qy     258 SWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE-----MLISKFR 306
      | :| | || | :|| :|| : : :| :| : ||:|
Db     264 PTLPCPTLQAFAIAYKCTRPFASMNSVLDPILFYFTQRKFRESTRYLLDKMSSKWR 319
```

RESULT 14

P2Y2_HUMAN

ID P2Y2_HUMAN STANDARD; PRT; 377 AA.
AC P41231; Q96EM8;
DT 01-FEB-1995 (Rel. 31, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE P2Y purinoceptor 2 (P2Y2) (P2U purinoceptor 1) (P2U1) (ATP receptor)
DE (Purinergic receptor).
GN P2RY2 OR P2RU1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Airway epithelium;
RX MEDLINE=94211846; PubMed=8159738;
RA Parr C.E., Sullivan D.M., Paradiso A.M., Lazarowski E.R., Burch L.H.,
RA Olsen J.C., Erb L., Weisman G.A., Boucher R.C., Turner J.T.;
RT "Cloning and expression of a human P2U nucleotide receptor, a target
RT for cystic fibrosis pharmacotherapy.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3275-3279(1994).
RN [2]
RP REVISIONS.
RX MEDLINE=95108098; PubMed=7809171;
RA Parr C.E., Sullivan D.M., Paradiso A.M., Lazarowski E.R., Burch L.H.,
RA Olsen J.C., Erb L., Weisman G.A., Boucher R.C., Turner J.T.;
RT "Cloning and expression of a human P2U nucleotide receptor, a target
RT for cystic fibrosis pharmacotherapy.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:13067-13067(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;

RA Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney, and Leukocyte;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that
 CC activate a phosphatidylinositol-calcium second messenger system.
 CC The affinity range is UTP = ATP > ATP-gamma-S >> 2-methylthio-ATP
 CC = ADP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Spleen, testis, kidney, liver, lung, heart and
 CC brain.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; U07225; AAC04923.1; -.
 DR EMBL; AY136753; AAN01279.1; -.
 DR EMBL; BC012104; AAH12104.1; -.
 DR EMBL; BC028135; AAH28135.1; -.
 DR HSSP; P34996; 1DDD.
 DR Genew; HGNC:8541; P2RY2.
 DR MIM; 600041; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0006873; P:cell ion homeostasis; TAS.
 DR GO; GO:0007200; P:G-protein signaling, coupled to IP3 second . . .; TAS.
 DR InterPro; IPR000276; GPCR_Rhodpsn.

DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE P2Y purinoceptor 4 (P2Y4).
 GN P2RY4 OR P2Y4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RA Bogdanov Y.D., Wildman S., King B.F., Burntock G.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=98421785; PubMed=9751165;
 RA Webb T.E., Henderson D., Roberts J.A., Barnard E.A.;
 RT "Molecular cloning and characterization of the rat P2Y4 receptor";
 RL J. Neurochem. 71:1424-1434(1998).
 CC -!- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that
 CC activate a phosphatidylinositol-calcium second messenger system.
 CC Not activated by ADP or UDP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Widely expressed at low levels. In brain,
 CC higher expression in the pineal gland and ventricular system.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC -----
 DR EMBL; Y14705; CAA75007.1; -.
 DR EMBL; Y11433; CAA72241.1; -.
 DR HSSP; P34996; 1DDD.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 91 2 (POTENTIAL).
 FT DOMAIN 92 108 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 109 127 3 (POTENTIAL).
 FT DOMAIN 128 149 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 150 170 4 (POTENTIAL).
 FT DOMAIN 171 192 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 193 218 5 (POTENTIAL).
 FT DOMAIN 219 242 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 243 265 6 (POTENTIAL).
 FT DOMAIN 266 283 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 284 305 7 (POTENTIAL).
 FT DOMAIN 306 361 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 104 181 BY SIMILARITY.
 FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 361 AA; 40893 MW; 0377F96E54B449A3 CRC64;

Query Match 21.5%; Score 354; DB 1; Length 361;
 Best Local Similarity 30.6%; Pred. No. 1.9e-16;
 Matches 86; Conservative 60; Mismatches 125; Indels 10; Gaps 5;

QY 26 YAIEFIFGLLGNVTVVFGYLFCKMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY-ANDKG 84
 ||: |: || | :: :|| :: |:: |::|::|| :: :|| |: | | :
 Db 38 YAVVFLGLALNAPTLWLFLFRLRPWDATATYMFHLALSDTLYVLSLPTLVYYYAARNHW 97
 QY 85 TYGDVLCISNRYVLHTNLTYLSILFTLFISMDRYLLMKYPFREHFLQKKEFAILISLAVWA 144
 :| || |:: : || |::|:: ||: ||| : :| | : || |: | ||
 Db 98 PFGTGLCKFVRFLFYWNLYCSVFLTCISVHRYLGICHPLRAIRWGRPRFASLLCLGVWL 157
 QY 145 LVTLEVLPMPLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLSVMCFFYY 204
 :| ::| | |: : | | :| : :| : :| | :| : |
 Db 158 VVAGCLVPNLFFVTNANGTTILCHDTTLPEEFDHYVFSSAVMVLLFGLPFLITLV CYG 217
 QY 205 KVVFLKR---RSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIASRLDSWPQ 261
 | | | : | :: | : | : : :|:: | |::| | : :||
 Db 218 LMARRLYRPLPGAGQSSSRL---RSLRTIAVVLTVFAVCFVPFHITRTIYYQARL--LQA 272
 QY 262 GC-TQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
 | : :| :| || | || ::| : | || | |
 Db 273 DCHVLNIVNVVYKVTRPLASANSCLDPVLYLFTGDKYRNQL 313

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 Job time : 27 secs